Schreiber, David

From: Sent: To:

Ramirez, Delia Tuesday, December 09, 2003 12:00 PM Schreiber, David case 09/843,250

Subject:

Hi,

I would like to request the following interference searches: seq id 2, 26, 32, 33, 34, 35, 36 in the protein databases.

Thank you,

Delia M. Ramirez, Ph.D. Patent Examiner Recombinant Enzymes-Art Unit 1652 1911 S. Clark Street, Crystal Mall 1, 10D06, Mail room 10D01 Ařlington, VA 22202 (703) 306-0288 delia.ramirez@uspto.gov

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December 9, 2003, 15;44:14 ; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec
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Sequence 35,
Sequence 26,
Sequence 59,
Sequence 18,
Sequence 17,
Sequence 17,
Sequence 17,
Sequence 18,
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                                                                                                                                                                                          2408
1 MNYANKILVSESGLSQKHLI......ARFEHASSTWHTELTKTTDR 449
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Sequence
Sequence
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_MBW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_NBW PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NBW PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_NBW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NBW PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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13: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US108_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US108_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-843-250-14
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US-09-843-250-59
US-09-843-250-16
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                                                                                                                                                                                                                                                                                                   684280 seqs, 185983659 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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        US-09-843-250-21
        Sequence 20, Appl 18

        19
        2219
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        11
        US-09-843-250-22
        Sequence 21, Appl 19

        20
        1968.5
        81.7
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        11
        US-09-843-250-23
        Sequence 23, Appl 20

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        US-09-843-250-24
        Sequence 23, Appl 20

        21
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        15.6
        483
        9 US-09-815-242-11692
        Sequence 1053. Appl 20

        22
        375.5
        15.6
        489
        9 US-09-815-242-11692
        Sequence 1053. Appl 20

        23
        375.5
        15.6
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        9 US-09-815-242-11692
        Sequence 1053. Appl 20

        24
        31
        US-09-815-242-11692
        Sequence 11692. Appl 30
        Sequence 11692. Appl 30

        25
        14.0
        424
        9 US-09-776-490-19
        Sequence 11692. Appl 30

        26
        17.7
        35
        9 US-09-776-490-12
        Sequence 11, Appl 30

        27
        35
        9 US-09-776-490-12
        Sequence 21, Appl 30

        31
        11.0
        4.6
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ALIGNMENTS

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APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Lee, K.
APPLICANT: Lee, K.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the TITLE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: PCT/US99/25079
PRIOR PILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Pastern OF Windows Version 4.0
SEQ ID NO 33
LENGTH: 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2408; DB 11; Length 449;
100.0%; Pred. No. 1.5e-225;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:28
                Sequence 33, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%
Matches 449; Conservative
US-09-843-250-33
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Qy 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERINKEIGDVRABITYRSHLMCTV 300 Db 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERINKEIGDVRABITYRSHLMCTV 300 Qy 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGFWES 360 Db 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGFWES 360 Qy 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 Qy 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 Db 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 NG-09-843-250-14 5 Sequence 14 Application 15	APPLICANT: Lee, K. TITLE OF INVENTION: NO. US2003; FILE REFERENCE: 875.006US2 CURRENT APPLICATION NUMBER: US. CURRENT FILING DATE: 2001-04-04-08-08-08-08-08-08-08-08-08-08-08-08-08-	Query Match 99.8%; Score 2404; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 3.7e-225; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 MNYNNKILVSESGLSQKHLHGDEELPQHELKTIFARNWLFLTHDSLIPAPGDYYTAKNG 60	QY 61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 DD 61 IDEVIVSRQNDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVFFE 120 QY 121 KDLYGESLNKKCLGIKEVARVESFHGFTYGCFDQRAPPLMDYLGDAAMTLEPMFKHSGGL 180 DD 121 KDLYGESLNKKCLGIKEVARVESFHGFTYGCFDQRAPPLMDYLGDAAMTLEPMFKHSGGL 180	QY 181 ELVGEPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 DD 181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 QY 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELNAFGGAKQERLNKEIGBVRARIYRSHLNCTY 300 DD 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELNAFGGAKQERLNKEIGBVRARIYRSHLNCTY 300 CQY 301 FPINNSMLTCSGVFKVWNPIDANTTBVWTYAIVEKOMPEDLKRRLADSVQRTAGPAGFWES 360 DD 301 FPINNSMLTCSGVFKVWNPIDANTTBVWTYAIVEKOMPEDLKRRLADSVQRTYGPAGFWES 360 CQY 301 FPINNSMLTCSGVFKVWNPIDANTTBVWTYAIVEKOMPEDLKRRLADSVQRTYGPAGFWES 360 QY 361 DDNDNWETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
121 KDLYGESLNKKCLGLKEVARVESFHGFLYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 121 KDLYGESLNKKCLGLKEVARVESFHGFLYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 121 KDLYGFSLNKKCLGLKEVARVESFHGFLYGCFDQBAPPLMDYLGDAAWYLEPWFKHSGGL 180 181 ELVQPPGKVYLKANKKAPAENFYGGAYLVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 181 ELVQPPGKVYLKANKKAPAENFYGGAYLVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 181 ELVGPPGKVYLKANWKAPAENFYGGAYLVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 241 QWTSKYGSGMGVLMPGYSGYHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 1	ω κι ον	346. FO	Query Match Best Local Similarity 99.8%; Pred. No. 3.7e-225; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Qy MNYNNKILVSESGLSQKHLIHGDEELPQHELKTIFARNWLFTHDSLIPAPGDYVTAKMG 60	

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Sequence 32, Application US/09843250;
Publication No. US2003022335A1;
General INFORMATION:
APPLICANT: Parales, R.;
APPLICANT: Resnick, S.;
APPLICANT: Resnick, S.;
APPLICANT: Resnick, S.;
APPLICANT: Resnick, S.;
APPLICANT: Besnick, S.;
APPLICANT: Wow Wers. US/09/843,250;
CURRENT FILING DATE: 1999-10-26;
PRIOR APPLICATION NUMBER: US 60/105,575;
PRIOR APPLICATION NUMBER: US 60/105,575;
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PastSEQ for Windows Version 4.0;
SEQ ID NO 32
LENGTH: 449
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Publication No. US20030022335A1
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the
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                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.8 Matches 448; Conservative
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US-09-843-250-34
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                                                                                                                                                                        Sequence 15, Application US/09843250

Sequence 15, Application US/09843250

Publication No. US20030022335A1

APPLICANT: Parales, R.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

APPLICANT: Leo, K.

TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2

CURRENT APPLICATION NUMBER: US/09/843,250

CURRENT PILING DATE: 1999-10-26

PRIOR PLILING DATE: 1999-10-26

PRIOR PLILING DATE: 1999-10-26

PRIOR PLILING DATE: 1999-10-26

PRIOR PLILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 65

SOFTHARE: PastSEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 449
300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:4.03-09-843-250-15
                                                           449
                                                                              OAHVSSSNWABFEHASSTWHTELTKTTDR 449
                                                      OAHVSSSNWAEFEHASSTWHTELTKTTDR
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ORGANISM: Artificial Sequence
                                                                                                                                            RESULT 4
US-09-843-250-15
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APPLICANT: Barales, R.
APPLICANT: Gibson, D.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the TILE OF INVENTION: NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: DCT/US99/25079
FRIOR FILING DATE: 1999-10-26
FRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 449
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                                                                            ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:30 US-09-843-250-35
                                                                                                                             Score 2403; DB 11;
Pred. No. 4.6e-225;
0; Mismatches 1;
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Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                                                                               99.84;
                          LENGTH: 449
TYVE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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ORGANISM: Artificial Sequence
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            SEO ID NO 35
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                                                                                                                                                                                                                                                      99.8%; Score 2404; DB 11; Length 449; 99.8%; Pred. No. 3.7e-225; live 0; Mismatches 1; Indels 0
                                                                                                                                                                                                         CTHER INFORMATION: A polypeptide encoded by SEQ ID NO:29-08-09-843-250-34
FILE REPERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
FRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR PILING DATE: 1999-10-26
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PSSLERQ for Windows Version 4.0
LENGTH: 449
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 99.8<sup>1</sup>
Matches 448; Conservative
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US-09-843-250-35
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APPLICANT: Barales, R. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Gestick, S. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the FILE REFERENCE: 875,006USZ CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT FILING DATE: 1999-10-26 PRIOR APPLICATION NUMBER: PCT/US99/25079 PRIOR FILING DATE: 1999-10-26 PRIOR FILING DATE: 1998-10-26 NUMBER OF SEQ ID NOS: 65 SOFTHAME: PCT/US WINDOWS Version 4.0 SEQ ID NOS: 65 LENGTH: 449
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  121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQBAPPLMDYLGDAAWYLBPMFKHSGGL 180
                             121 KOLYGESINKKKCLGIKEVARVESFHGFIYGCPOORAPPLMDYLGDAAWYLEPPRKHSGGL 180
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ORGANISM: Artificial Sequence
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US-09-843-250-59
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US-09-843-250-26

US-09-843-250-26

Sequence 26. Application US/09843250

Publication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Parales, R.

APPLICANT: Resnick, S.

APPLICANT: Lee, K.

TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US

CURRENT APPLICANTON NUMBER: US/09/843,250

CURRENT FILING DATE: 2001-04-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1998-10-26

WUMBER OF SEQ ID NOS: 65

WUMBER OF SEQ ID NOS: 65
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                                                                                                                                                                                                                                                         KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAMYLEPMFKHSGGL 180
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                                                                                                1 MNYNNKILVSESGLSQKHLIHGPEELPQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
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                                                                     1 MAYANAKILVSESGLSQXHLIHGDEELFQHELXTIPARNWLFLTHDSLIPAPGDYVTAXONG
                                                                                                                                                                                                                                                                                                                                                     181 BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
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                           1; Indels
99.8%; Pred. No. 4.6e-225; tive 0; Mismatches 1;
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Best Local Similarity 99.84
Matches 448; Conservative
                      Matches 448; Conservative
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ORGANISM: Pseudomonas sp.
Best Local Similarity
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LENGTH: 449
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General Information US/09843250

| Sequence 16, Application US/09843250
| Publication No. US20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Parales, R. APPLICANT: Cash K. APPLICANT: Lee, K. APPLICANTON: NO. US20030022335A1el naphthalene dioxygenase and methods for the PRIB REFERENCE: 875.006US2
| CURRENT PRILING DATE: 2001-04-26
| PRIOR PRILING DATE: 1999-10-26
| PRIOR PLING DATE: 1998-10-26
| PRIOR PLING DATE: 1998-10-
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361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGBDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                      421 QAHVSSSNWARFEHASSTWHTELTKTTDR 449
                                                                                                            421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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ORGANISM: Artificial Sequence
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US-09-843-250-16
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US-09-843-250-17
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APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: NO. USZOG30022335Alel naphthalene dioxygenase and methods for the FILE REPERBYCE: 875.006USZ
CURRENT APPLICATION NUMBER: US/09/443,250
CURRENT FILING DATE: 1999-10-26
PRIOR PILING DATE: 1999-10-26
RIOR PILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
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       241 QMTSKYGSGWGVLWDGYGGVHSADLVPBLMAFGGAKQBRLNKEIGDVRARIYRSHINCTV 300
                                                                                                            301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWES 360
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US-09-843-250-58
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US-09-843-250-58
; Sequence 58, Application US/09843250
; Publication No. US20030022335A1
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LENGTH: 449
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APPLICANT: Parales, R. APPLICANT: Parales, R. APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Resnick, S. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE OF INVENTION NUMBER: US/09/843,250 CURRENT APPLICATION NUMBER: US/01-04-26 PRIOR APPLICATION NUMBER: US 60/105,575 PRIOR APPLICATION NUMBER: US 60/105,575 NUMBER OF SEQ ID NOS: 65 SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MNYKNKILVSESGGJTQKHLIHGDESLFQHSLRTIFARNWLFLTHDSLIPSPGDYVTAKNG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNYMNKIIVSESGESQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIFAPGDYVTAKMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.4%; Score 2346; DB 11; Length 449; Best Local Similarity 96.7%; Pred. No. 1.6e-219; Matches 434; Conservative 10; Mismatches 5; Indels 0
                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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                     CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1999-10-26
PRIOR PILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PSESEQ for Windows Version 4.0
SOFTWARE: 449
     CURRENT APPLICATION NUMBER: US/09/843,250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 19, Application US/09843250
; Publication No. US20030022335A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence PRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-843-250-19
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                                                                                                                                                                                                                                                             TYPE: PRT
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Publication No. US20030022335A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Paralos, R.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875,006US2
                                                                                                       APPLICANT: Gibson, D.
APPLICANT: Resultck, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 DDNDNMETASQNGKKYQSRDSDLASNLGPGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IDEVIVSRQNDGSIRAFLAVVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVFFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 99.4%; Score 2394; DB 11; Length 449; Best Local Similarity 99.3%; Pred. No. 3.5e-224; Matches 446; Conservative 1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTHER INFORMATION; A polypeptide encoded by SEQ ID NO:6.
US-09-843-250-17
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CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
Sequence 17, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                 APPLICANT: Parales, R. APPLICANT: Gibson, D.
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LENGTH: 449
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241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVPARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                              61 IDBVIVSRQSDGSIRAFINVCRHRGKTLVNAEAGNAKGFVCSYHGMGFGSNGELQSVPFE 120
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                                                                                                                                                                                                                                         61 IDEVIVSRONDGSIRAFLAVCRHRGKTLVSVERGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                       241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGÐVRARIYRSHLNCTV 300
                                                                                                                                                                                    0; Gaps
                                                                                                                                 Query Match 96.3%; Score 2318; DB 11; Length 449; Best Local Similarity 95.5%; Pred. No. 8.7e-217; Matches 429; Conservative 12; Mismatches 8; Indels 0.
                                        OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:8.
NAME/KEX: SITE
I LOCATION: (35)...(35)
OTHER INFORMATION: Xaa = any amino acid.
US-09-843-250-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
LENGIH: 449
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Search completed: December 9, 2003, 16:09:33 Job time: 23.1429 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 MNYNNKIIVSESGLSQKHLI.....ABFEHASSTWHTELTKTTDR 449 Total number of hits satisfying chosen parameters: 328717 segs, 42310858 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 US-09-843-250-34 Perfect score: Scoring table: Sequence: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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/cgm2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgm2_6/ptodata/1/iaa/6TCOMB.pep:*
/cgm2_6/ptodata/1/iaa/ptmys_COMB.pep:*
/cgm2_6/ptodata/1/iaa/ptmys_COMB.pep:* Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Issued Patents AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 31367, A		Sequence 7248, Ap					4700,	13	Sequence 4, Appli	ď	13	20,				Sequence 4, Appli			14,	Sequence 13, Appl	15,	4	Sequence 16, Appl	16,	Sequence 16, Appl	16,
αı	US-09-252-991A-31367	US-09-328-352-6452	US-09-328-352-7248	US-09-252-991A-31385	US-09-328-352-7581	US-09-252-991A-25088	US-09-252-991A-17164	US-09-328-352-4700	US-09-252-991A-19627	US-09-004-393B-4	US-09-004-393B-2	US-08-810-009-19	US-08-810-009-20	US-08-810-009-21	US-09-252-991A-27100	US-09-328-352-6765	US-08-976-063E-4	US-09-028-934-36	US-08-810-009-12	US-08-810-009-14	US-08-810-009-13	US-08-810-009-15	US-09-311-626B-4	US-08-809-326A-16	US-09-689-914A-16	US-09-689-913A-16	US-09-689-916A-16
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Query Match Length DB	463	496	445	466	471	425	449	375	529	446	439	35	35	35	629	392	354	379	35	35	35	35	622	432	432	432	432
Query Match	16.9	16.9	16.1	15.9	14.9	14.3	12.1	11.6	6.6	6.9	9.3	7.7	7.5	7.0	9	5.3	4.9	4.7	4.6	4.5	4.5	4.5	4.5	4.4	4.4	4.4	4.4
Score	407.5	407.5	388	382.5	360	344.5	291	278.5	237.5	224	223	185	174	168	143.5	128	118.5	113.5	110	109	108	108	108	106.5	106.5	106.5	106.5
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Sequence Sequence Sequence	Sequence Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence	Sequence Sequence Sequence Sequence
US-08-809-326A-15 US-09-689-914A-15 US-09-689-913A-15	US-09-689-916A-15 US-08-810-009-9 US-09-328-352-4956 US-08-810-009-18	US-08-810-009-11 US-08-810-009-8 US-08-810-009-10	US-08-8IO-009-44 US-08-8IO-009-45 US-09-198-452A-466 US-09-198-452A-466	US-08-810-009-17 US-09-325-932A-57 US-09-252-991A-28371 US-09-134-001C-4800
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AL IGNMENTS

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APPLICUAT: MAIC J. Rubenfield et al.
APPLICUAT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGUINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV--PFEKDLYGESLANKKCLG---LKE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 VARPESYRGFLFGSINPDVRPLAEHLGBSAKIIDMIVDQSPBGLEVLRGSSSYVYRGNWK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 APAENFVGDAYHVG---WTHASS------LRSGESIFSSLAGNAALPPEGAGLQ 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 LTAEN-GADGYHVSSVHWNYAATOSQRQQRDAADPLRT-----MSAAGWAR---QGGGFY 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 MTSKYGSGMGVLWDGYSGVHSADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCT 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 DPRLFELEMKHIFEGNWYYLAHESQVAGVNDYLTTQIGRQSIVIARNBGQLNAFINACS 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery March 16.9%; Score 407.5; DB 4; Length 463; Best Local Similarity 29.0%; Pred. No. 1.2e-30; Matches 110; Conservative 69; Mismatches 149; Indels 51;
                                             ; Sequence 31367, Application US/09252991A; Patent No. 6551795; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-252-991A-31367
                            US-09-252-991A-31367
RESULT 1
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RESULT 4

US-09-222-91A-31385

J Squence 31385, Application US/09252991A

Fatent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

PILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 31385
                                                                                                                                                                                                                                                                    165 RVBEYNGMIPASFKEDIOPLESFLGPAKKWIDLFMKOGAGYPIKVLGBHRFRFPG---- 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 QPGFVEDLGNGHSVMVMIPELVDLEEDLMERPIQERFEDLAQALRDEGHEBLEVRRIVRA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 ---SHINCTVFPNNSMLTCS-GVFKVWNPIDANTTEVWTYAIVEKD----MPEDLKRRLA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 VGGSGFNLNLFPN---IACSMAFFRVLOPISVAETEI-HHSVITMDGGPQIANQYRLRLH 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 EHFQ----CPFGFGTPDDSEAWERV-QHCAN-AGNDLWIMINRGL-------PGEVKT 418
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                                                                                                                                                                            107 RCHHRAATVCEHKKGKTNSFVCPYHGWSYALDGSLRGVP-SPESYGDCLDKSELPLVSL- 164
                                                                                                                                                                                                                                        140 RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGG--LELVGP-----PGKVVIK 192
                                                                                                                                                                                                                                                                                                                                               193 ANWKAPABNFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLQWTSKYGS 248
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                                                                                                                                                                                                                                                                                                                                                                                                   220 -NWKIQLEN-TTDAYHFPLVHKSFLSSVDEKTEBLFN--------FFRN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 IHGDBELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDBVIVSRQNDGSIRAFLN 79
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15.9%; Score 382.5; DB 4; Length 466;
Best Local Similarity 27.1%; Pred. No. 3.2e-28;
Matches 120; Conservative 77; Mismatches 182; Indels 63.
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/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31385
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Sequence 7248 Application US/09328352
Patent No. 6562958
GRUREAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7248
ILBRGTH: 445
                                                                                                                                                             Sequence 6452, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Braton et al.
APPLICANT: GATY L. Braton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 HRGKTLVSVEAGNAKGFVÇSYHGWGFGSNGBLQSVPFBKDL-YGESLNKK-CLGLKEVAR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 VESFHGFIYGCFDQEAPPLMDYLGDAAWYLBPMFKHS-GGLELVGPPGKVVIKANWKAPA 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 EN-GADGYHVSAVHWNYAATTQHRKE--TQAADNIRAMSAGSWGKQGGGSYGFENGHMLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 WDGYSGVHSADLVPELMAPGGAKQBRLNKEIGDVRAR--IYRSHLNCTVFPNNSMLTCSG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
16.9%; Score 407.5; DB 4; Length 496; .
Best Local Similarity 31.3%; Pred. No. 1.4e-30;
Matches 105; Conservative 59; Mismatches 146; Indels 25; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 SQIRVLRPLSVNRTEVIIYCIAPKGEAPEARARI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312 -VEKVWNPIDANTTEVWTYAIVEK-DMPEDLKRRL 344
                               374 TPDDLEBFRSCQQG---YQ 389
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US-09-328-352-7248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6452
359 ESDDNDNMETASONGKKYQ 377
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US-09-328-352-7248
                                                                                                                                                     US-09-328-352-6452
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LENGTH: 496
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Sequence 25088, Application US/09252991A
Parent No. 6551795
GENERAL INFORMATION
FAURINGLIANT: MARC U. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US/09/252,991A
PRIOR PRICATION NUMBER: US/09/25186
PRIOR PRICATION NUMBER: US/09/218
PRIOR FILING DATE: US/09/2190
PRIOR FILING DATE: US/09/2190
PRIOR FILING DATE: US/09/2190
PRIOR FILING DATE: US/09/2190
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: 107196.136
FILE REPREBACE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 14.3%; Score 344.5; DB 4; Length 425;
Best Local Similarity 27.4%; Pred. No. 1.2e-24;
Matches 114; Conservative 71; Mismatches 178; Indels 53; Gaps 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 DILGIN--IRSFFPTAADEVSVTVWGAGFADETREERAARINGLISFIGPGGFGTPDDVE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GKTLVSVBAGNAKGFVCSYHGWGFGSNGELQSVÞFEKDLYGESLNKKCLGLKEVARVES- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 -FHGFIYGCFDQBAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAEN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 VYRNFLFIHYAARQPSLETYLGQAKDYIDLICDQSEAELEIIPGGFEHSIKANWKLLAEN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 FVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202 GV-DAYHLPPAHKRYLEYLNTL------GTDPESHKRHGRG-BALGNGHALII 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ELHRRELHEIFODSWLYAAHLSELREPGDFIITRDVGGRNLIIQRRADGEPAVYLNACAHR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 S------ADLVPE-LMAFGGAKOBRINKBIGDVRAR-IYRSHINCTVFPN---N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           365 ILESCO---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREW 407
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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// Patent No. 6551795
// GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25088
                                                                                                             US-09-252-991A-25088
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LENGTH: 425
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### REPREMAL INFORMATION:

### TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

### TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

### TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

### CURRENT APPLICATION NUMBER:

### CURRENT FILING DATE: 1999-06-04

### NUMBER OF SEQ ID NOS: 8252

### ENDIAGNOSTICS

### E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     263 DGWFGFKNGHSVLFSDMPNFTVRPGYSTVMPYMVEKYGEKYAEWAMHRLRNLNLYPSLFF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L-TCSGVPKVMNPIDANTTEVWTYAIVEKOMPEDLKRRLADSVQRTTGPAGFWESDDNDN 365
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215 QNEWGL-DGYHVSTVHYNYV-----ATVQHRQQVEAERGGVAATLDYSKTGAGDAATD 266
                                                                                                             254 --WDGYSGVHS-------ADLYPELMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                                                            267 DGWFSPANGHSVLFSEMPNPAVRPGYASVMPRLVA-----EYGQARAEMMARRL 315
                                                                                                                                                                                                                                                             297 - NCTVFFNNSML-TCSGVFKVMNFIDANTJEVWTYAI-VEKDMPEDLKRRLADSVQRTTG 353
                                                                                                                                                                                                                                                                                                        316 RNIALIVPSLFVIDQISSQLRIVRPLAWNRTEIVSQCIGVKGESDADRENRIR-OFEDFFN 374
                                                                                                                                                                                                                                                                                                                                                                                                          354 PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAI---GE 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                    375 VSGMGTPDDLVEFREAQRGFQARLERNSDI.--SRGHGKWLEGATPNSQALGIAPLLIGTE 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            : [ [ :: [ :: [ :: ]: ]: ] : ] : ] : BPELFDLEMEFIFEKUMIYACHESEIPNNHDFLTVQIGRQPIIVSRDGKGELHAMVNACE 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLAVVCR 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Score 360; DB 4; Length 471; 25.9%; Pred. No. 4.6e-26; tive 69; Mismatches 181; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323 MDQISSQLRIVRPVAWNKTEV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 TSYRGFYRAYQAHVSSSNWAEF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            433 ITHEGLYVNQHAH-----WRRF 449
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US-09-328-352-7581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 25.84
Matches 114, Conservative
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US-09-328-352-7581
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Sequence 19627, Application US/09252991A

Factor No. 6551795

GENERAL INFORMATION:

FAPPLICATION

TITLE OF INVENTION:

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/252,991A

TRIDE APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

FRIOR PELING DATE: 1999-02-18

FRIOR PELING DATE: 1998-02-18

FRIOR PELING DATE: 1998-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-02-18

FRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 529
        191 IK--ANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLOMTSKYGS 248
                                                                                    249 GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKBIGDVRARIYRSHINCTVF---PNNS 305
                                                                                                               232 TTHQNWTLQYG------FARSSEKSFKLDPSVTDPEFHGFWT-WPCTMFNVPPGGN 280
                                                                                                                                                                                                 --- PGFADSVQVDKYWH 231
                                                                                                                                                                 306 MLICSGVFKVWNPIDANTIEVWTYAIV------EKDM------PEDLKRRLADS 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
9.9%; Score 237.5; DB 4; Length 5
Best Local Similarity 24.9%; Pred. No. 3.3e-14;
Matches 86; Conservative 54; Mismatches 139; Indels
                                 Sequence 4, Application US/09004393B
Patent No. 6310271
GENERAL INFORMATION:
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US-09-004-393B-4
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Patent No. 6562958
GRAKEAL INFORMATION:
PAPLICANT: GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GT99-03P8
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER: OF SEQ ID NOS: 8252
SEQ ID NO 4700
LENGTH: 375
                                                                                                                                                                                                                                                                            83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVF 142
                                                                                                                                                                                                                                                                                                                                                                                   227 LVIEN-NRECYHCNGSHPELLK-----TLLEMDDVTDPRAS--QAFKDQVAACTSAWD- 276
                                                                                                                                                                                                                          |: ||: ::: || : || DORLEBIDMORIFHKEWLIAGMTCEIPAKGNFLTLQIGKNPVLVIRGAEGQVHAFHNVCR 119
                                                                                                                                                                                                                                                                                                          143 SFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMPKHSGGLELVGPPGKVVIK-----ANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                        197 APAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 YSGVHSADLVPELMA-FG----------GAKQ---ERLINKEIGDVRA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 RIYRSHINCTVFPNNSMLTCSG---- JFKVWNPIDANTTEVWTYAIVEKDMPB----- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       331 ----IHI-------PHSWNHCMGDHLIVETVW-PISAQETLVTIKWLVHKDAVEGVDYDVA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               339 -----DLKRRLADSVQRTTGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 RLREVWDATNDQDRRLABENQRGINSDAYQPGPYSKTYEFGVINFLDWYS--ERWLANLG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFV-CSYHGWGFGSNGELQSV-----PFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 LINGDEBLEGHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDBVIVSRQNDGSIRAFL 78
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                                                                                                                 Query Match 12.1%; Score 291; DB 4; Length 449; Best Local Similarity 26.4%; Pred. No. 1.8e-19; Matches 111; Conservative 53; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Acinetobacter baumannii
US-09-328-352-4700
                                   ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17164
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Best Local Similarity
Matches 97; Conserv
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US-09-328-352-4700
SEQ ID NO 17164
                LENGTH: 449
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APPLICANT: Hanson D., Andrew
APPLICANT: Rathinashapathi, Bala
APPLICANT: Rathinashapathi, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
FILE REPERRICE: UP-1c2
CURRENT APPLICATION NUMBER: US/09/004,393B
CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/035,147
PRIOR APPLICATION NUMBER: 60/035,147
PRIOR APPLICATION NUMBER: 09/035,147
PRIOR PILING DATE: 1997-01-08
SUPPRARE: Patentin Ver. 2.0
SSQ ID NO 2
IENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 EDALIPPSTRYTEPARYSHELERIFYKGWQVAGYSEQVKEKNQYRIGSLGNVEYLVSKDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 KELGLAPL-KVAEWGPFILLISLDRSLDANADVGTEWIGKSAEDVKAHAFDPNLKFTHRSE 274
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APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polynuclectides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
TITLE OF INVENTION: Plants Transformed Therewith
TITLE OF INVENTION: Plants Transformed Therewith
CURRENT APPLICATION NUMBER: US/09/004,393B
CURRENT FILING DATE: 1999-01-08
PRIOR FILING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 9.3%; Score 224; DB 4; Length 446; Best Local Similarity 27.4%; Pred. No. 5e-13; Matches 58; Conservative 37; Mismatches 97; Indels
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9.3%; Score 223; DB 4; Length 439;
Best Local Similarity 30.1%; Pred. No. 6.1e-13;
Matches 58; Conservative 38; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
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                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Beta vulgaria
                                                                                                                                                                                                                                                                                                                                                                                                            US-09-004-393B-4
                                                                                                                                                                                                                                                                                                                                  LENGTH: 446
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147 FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                                                        APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE BELL, SELLZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 621437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
GENERAL TO GENERAL S.
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: GASY, John
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC Compatible
COMPUTER: PLOPS MS-DOS
SOFTWARE: PATENTIN FELEAGE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. MALTRAY
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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ilarity 94.3%; Pred. No. 5.6e-11;
Conservative 1; Mismatches 1;
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                                                                                                                                                                                                                                                        Sequence 19, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 577
TELECOWNUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-881-3175
TELEX: 575.102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTER.STICS:
LENGTH: 35 amino acids
                                                                                           201 NFVGDAYHVGWTH 213
                                                                                                                                       280 NYLDSSYHVPYAH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
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Best Local Similarity
Matches 33; Conserva
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TOPOLOGY: 1:
                                                                                                                                                                                                                                    15-08-810-009-19
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79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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7.0%; Score 168; DB 3;
Best Local Similarity 80.0%; Pred. No. 2.4e-09;
Matches 28; Conservative 3; Mismatches 4
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27100
              REFERENCE/DOCKGT NUMBER: 57
TELEMONINICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                               21:
                                                                         TELERA: 919-881-3175
TELEX: 575102
INPORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-21
                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS:
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US-09-252-991A-27100
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APPLICANT: Briggs, Steven P.
APPLICANT: Briggs, Steven P.
APPLICANT: Gray, John
TITLE OF INVENTION: GELD DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: CELD DEATH AND DISEASE RESISTANCE IN PLANTS
OUNDERS OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: US/08/81-3175
FILING DATE: US/08/81-3175
FILING CHARACTERISTICS:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: MIND DATES:
FILING DATE: US/08/810
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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NUMBER OF SEQUENCES: 65
CORRESSONNING ADDRESS:
ADDRESSBE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 21, Application US/08810009 Patent No. 6211437
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f TOPOLOGY: linear
j MOLECULE TYPE: protein
US-08-810-009-20
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US-08-810-009-21
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Patent No. 6551795
GENERAL INFORMATION:
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICANT:
APPLICANT:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION:
ARRIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 GIDEVIVSRONDGSIRAFLNVCRHRGK--TLVSVEAGNAKGFVCSYHGWGFGSNGELQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 PFEKDLYGESLNKKCLGLKEVAR--VESFHGFIY---GCFDQEAPPLMDYLGDAAWYLEP
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
6.0%; Score 143.5; DB 4; Length 6;
Best Local Similarity 24.3%; Pred. No. 4.6e-05;
Matches 65; Conservative 41; Mismatches 103; Indels
Length 35;
                                            Indels
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December 9, 2003, 15:44:14; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 34,
                                                                                                                                                                                                                         1 MNYNNKILVSESGLSQKHLI......AEFEHASSTWHTELTKTTDR 449
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1: /cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/RSO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-843-250-14
US-09-843-250-15
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US-09-843-250-19
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Maximum Match 100%
Listing first 45 summaries
                                                                       - protein search, using sw model
                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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20,	Sequence 21, Appl	22	Sequence 23, Appl	24	10253	Sequence 11692, A	Sequence 6140, Ap	Sequence 5097, Ap	7	Sequence 19, Appl		٠.	Sequence 20, Appl	Sequence 21, Appl	21	Sequence 4, Appli	12	12	14,	14,	13,	15,	13,	15,	4	Sequence 78, Appl	6	ď	Sequence 15, Appl
US-09-843-250-20		US-09-843-250-22	US-09-843-250-23		US-09-815-242-10253	US-09-815-242-11692		Þ		US-09-776-490-19	US-09-776-491-19	US-09-776-490-20	US-09-776-491-20	US-09-776-490-21	US-09-776-491-21	US-08-976-063C-4	US-09-776-490-12	US-09-776-491-12	-		US-09-776-490-13			-	US-10-124-880-4	US-10-047-542-78	US-09-776-490-9	US-09-776-491-9	US-09-924-097-15
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91	13	18	19	20	5	22	23	24	22	56	27	28	29	30	31	32	33	34	32	36	37	38	39	9	41	42	43	44	5

ALIGNMENTS

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APPLICANT: Barales, R.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Reservick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: NO. US20030022335Alel naphthalene dioxygenase and methods for the TILE REPERBENCE: 875.006092
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR PILING DATE: 1999-10-26
NUMBER OF SEC ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Score 2409; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 5e-226;
Matches 449; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:29. US-09-843-250-34
                      Sequence 34, Application US/09843250 Publication No. US20030022335A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
US-09-843-250-34
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OY 121 KOLYGRSINKKCIGLKEVARVESFHGFIYGGFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	Qy 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
Oy 181 ELVGPPCKVVIKANWKAPABNYVGDAYHVGMTHASSLRSGBSIFSSLAGNAALPPBGAGL 240	QY 301 PPNNSMLTCSGVFKVMNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWBS 360
241 QMTSKYGSGMGVLMDGYSGYBSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV [Qy 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDYYGDAVYPGVVGKSALGETSYRGFYRAY 420
301 PPNNSMLTCSGVFKVMNPIDANTTEVWTYALVEKOMPEDLKRRLADSVORTTGRAGFWES	Qy 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 Db 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
OY 361 DDNDNMETASONGKKYOSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	RESULT 3 US-09-843-250-14 ; Sequence 14, Application US/09843250
Qy 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 Db 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449	; FUBLICATION NO. USZUJSSAI ; GENERAL INFORMATION: ; APPLICANT: Barales, R. ; APPLICANT: Gibson, D.
RESULT 2 US-09-843-250-2 ; Sequence 2, Application US/09843250 ; Publication No. US20030022335A1 ; GENERAL INFORMATION: ; APPLICATION: ; APPLICATION:	
APPLICANT: Resnick, S. ; APPLICANT: Lee, K. ; TILE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the ; TILE REFERENCE: 975.006US2 ; CURRENT APPLICATION NUMBER: US/09/843.250	FRIOR APPLICATION NUMBER: US 60/105,575 PRIOR FILING DAIR: 1998-10-26 NUMBER OF SEQ ID NOS: 65 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH, 4.0
CURRENT FILING DATE: 2001-04-26 FRIOR APPLICATION NUMBER: PCT/US99/25079 FRIOR FILING DATE: 1999-10-26 FRIOR APPLICATION NUMBER: US 60/105,575 FRIOR APPLICATION NUMBER: US 60/105,575 MANABED OF SEC IT NOT 50	0-s
WOMBER OF SEQ ID NOS: 65 5 SOFTWARE: FastSEQ for Windows Version 4.0 5 SEQ ID NO 2 LENGTH: 449 7 TYPE: PRT	Query Match 99.8%; Score 2404; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 1.5e-225; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
	Qy 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLELTHDSELFAPGDYVTAKKG 60
Query Match 99.8%; Score 2404; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 1.5e-225; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gans 0;	Qy 61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
YNNKILVSESGLSOKHLIHGDEELPOHELKTIFARWLFLTHDSLIPAPGDY 	Qy 121 KOLYGESLNKKCLGIKEVARVESFHQFIYGCFDQBAPLMDYLGDAAWYLEDMFKHSGGL 180
	QY 181 ELVGPPGKVVIXANWKAPAENFVGDAYHVGWTHASSLRSGESIFSGLAGNAALPPEGAGL 240
	Qy 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
ELVGPPCKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGU 	Oy 301 PPNNSMLTCSGVFKVWNPIDANTTEVWTYALVEKDMPEDLKRRLADSVORTTGPAGFWES 360
	SOI DUNDNMBIASQNGAALQSADSULASNLASTGEDVIGDAVIYGVVGKSALGEISIKGFIKAY

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Sequence 33, Application US/09843250

Sequence 33, Application US/09843250

Sequence 33, Application US/09843250

SENDIAL INFORMATION:

APPLICANT: Parales, R.

APPLICANT: Resentck, S.

APPLICANT: Lee, K.

TILLOO INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006032

CURRENT APPLICATION NUMBER: US/09/843,250

CURRENT APPLICATION NUMBER: DS.

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 449

TYPE: PRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 OMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.8%; Score 2404; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 1.5e-225; Matches 448; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:28
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; Publication No. US20030022335A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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   US-09-843-250-33
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                                                                                                                                                                                                                                                                                            ## Sequence 15. Application US/09843250

| Sequence 15. Application No. US2003022335A1
| GENERAL INFORMATION:
| APPLICANT: Braines, R. |
| APPLICANT: Braines, R. |
| APPLICANT: Resnick, S. |
| APPLICANT: Lee, K. |
| FILE REFERENCE: 875.006U32
| CURRENT FILING DATE: 2001-04-26
| PRIOR PLILING DATE: 1999-10-26
| PRIOR PLILING DATE: 1999-10-26
| PRIOR PLILING DATE: 1999-10-26
| WUMBER OF SEQ ID NOS: 65
| SEQ ID NO 15
| LEAST RESERVED (F. Windows Version 4.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:4.
US-09-843-250-15
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US-09-843-250-15
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APPLICANT: Barales, R. APPLICANT: Gibson, D. APPLICANT: Research, S. APPLICANT: Research, S. APPLICANT: Research in the control of the control 
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                                                                                                                                                             ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:31. US-09-843-250-36
                                                                                                                                                                                                                                                   Query Match 99.8%; Score 2403; DB 11; Best Local Similarity 99.8%; Pred. No. 1.9e-225; Matches 448; Conservative 0; Mismatches 1;
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99.8%; Pred. No. 2.4e-225;
ive 0; Mismatches 1;
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Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity 99.8
Matches 448; Conservative
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US-09-843-250-26
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                  SEQ ID NO 36
LENGTH: 44
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| Sequence 36, Application US/09843250 |
| Publication No. US200300223351 |
| GENERAL INFORMATION: |
| APPLICANT: Gibson, D. |
| APPLICANT: Reanick, S. |
| APPLICANT: Lee, K. |
| TITLE OF INVANTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 |
| OURRENT PEDLICANTON NUMBER: US/09/843,250 |
| CURRENT PEDLICATION NUMBER: PCT/US99/25079 |
| PRIOR APPLICATION NUMBER: US 60/105,575 |
| PRIOR FILING DATE: 1999-10-26 |
| PRIOR FILING DATE: 1999-10-26 |
| PRIOR FILING DATE: 1999-10-26 |
| NUMBER OF SEQ ID NOS: 65 |
| NUMBER OF SEQ ID NOS: 65 |
| SOFTWARE: PastSEQ for Windows Version 4.0
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99.8%; Score 2403; DB 11; Length 449;
Best Local Similarity 99.8%; Pred. No. 1.9e-225;
Matches 448; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:30. US-09-843-250-35
PILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR PILING DATE: 1999-10-26
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTHARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 449
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                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-843-250-36
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GRNEAL INFORMATION:

APPLICANT: BAPALICATION US/09843250

Publication No. US2003002233541

SAPLICANT: PARALICAN:
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the TILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250

CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
SOFTWARE FASESEQ for Windows Version 4.0
SEQ ID NO 58
LENGTH: 449
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                                                                         ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
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               BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGBSIFSSLAGNAALPPEGAGL
                                                                                                                                                                       PPNNSMLTCSGVFKVWNPIDANTIEVWTYAIVEKDMPEDLKRRLADSVQRTTGPAGFWES
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                                                                                                               OMTSKYGSGMGVLMDGYSGVHSADLVPBLMAFGGAKQBRLNKBIGDVRARIYRSHLNCTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:56.
US-09-843-250-58
                                                                                                                                                                                                                                                                                                          QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-843-250-58
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FUDICATION:
APPLICANT: PAIR SAINCE, INCORNATION:
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Best K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.064052
CURRENT FILING DATE: 2001-04-26
PRIOR PILING DATE: 1999-10-26
PRIOR PLIING DATE: 1999-10-26
PRIOR PLIING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 449
                                                           IDEVIVERONDGSIRAFLANCRHRGKTLVSVEAGNAKGFVCSYHGNGFGSNGELQSVPFE 120
                                                                             BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
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                         KOLYGESLNKKCLGLKEVARVESFHGFLYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
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99.7%; Score 2402; DB 11; Length 449;
Best Local Similarity 99.8%; Pred. No. 2.4e-225;
Matches 448; Conservative 0; Mismatches 1; Indels 0
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ORGANISM: Artificial Sequence
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US-09-843-250-32
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Db 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELWAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 Qy 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTVAIVEKOMPEDLKRRLADSVORTTGPAGFWES 360 Bb 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTVAIVEKOMPEDLKRRLADSVORTTGPAGFWES 360 GY 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 Db 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QY 421 QAHVSSSNWAEPEHASSTWHTELTKTTDR 449 DD 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449	Db 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 Qy 421 QAHVSSSNWAEPEHASSTWHTELTKTTDR 449 Db 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 RESULT 12 US-09-843-250-16 'S Sequence 16, Application US/09843250 'Publication No. US20030022335A1 'GENERAL INFORMATION: 'A APPLICANT: Parales, R. 'A APPLICANT: Gibson, D.
RESULT 11 US-843-250-59 US-963-220-59 US-963-250-59 IS-843-250-59 IS-843-250-59 IS-843-250-59 IS-843-250-59 IS-843-250-59 IS-843-250-59 IS-843-250 IS-843-	### PRPLICANT: Resultck, S. ### APPLICANT: Lee, K. ### APPLICANT: Lee, K. #### APPLICANT: Lee, K. #### TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPERBNCE: 875.006US2 #### CURRENT APPLICATION NUMBER: US/09/843,250 #### CURRENT FILING DATE: 1999-10-26 #### PRIOR PILING DATE: 1999-10-26 #### PRIOR PILING DATE: 1999-10-26 #### PRIOR FILING DATE: 1999-10-26 #### PRIOR APPLICATION NUMBER: W 60/105, S75 #### SOFTWARE: PastSEQ for Windows Version 4.0 #### SEQ ID NO 16 #### INFORMATION: A polypeptide encoded by SEQ ID NO:5. #### US-09-843-250-16
OJ.	Query Match Best Local Similarity 99.6%; Pred. No. 4.7e-225; Matches 447; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
) ORGANISM: Artificial Sequence ; PRATURE: ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:57. US-09-843-250-59	Qy 1 MNYNNKILVSBSGLSQKHLIHGDEELPQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
Query Match Best Local & Matches 448	QY 61 IDEVIVSRONDGSIRAFLANCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 DD 61 IDEVIVSRQNDGSIRAFLANCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 DD 61 IDEVIVSRQNDGSIRAFLANCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 QY 121 KDLYGESLANKKCLGLKEVARVESFHGFTYGCFDQBAPLMDYLGDAAWYLEPMFKHSGGL 180
	DD 121 KDLYGESINKKCIGLKEVARVESFHGFIYGCFDQSAPPLMDYIGDAAMYLEPMFKHSGGL 180 QY 181 BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
	QY 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLMCTV 300 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLMCTV 300
	301 PPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKOMPEDLKRRLADSVQRTTGPAGFWES
241 OMISKYGSGMGYLMDGYSGYRSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV	
301	Db 421 QAHVSSSNWAEFEHASSTWHTBLTKTTDR 449
Qy 361 DDNDNMETASQNGKXYQSRDSDLISNTGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	RESULT 13 US-09-843-250-17

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Sequence 19, Application US/09843250;
Sequence 19, Application US/09843250;
Publication No. US20030022335A1
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Reanick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPRENCE: 875.0604022;
CURRENT APPLICATION NUMBER: US/09/843,250;
CURRENT PILING DATE: 1999-10-26;
PRIOR FILING DATE: 1999-10-26;
PRIOR FILING DATE: 1999-10-26;
PRIOR FILING DATE: 1999-10-26;
PRIOR FILING DATE: 1999-10-26;
NUMBER OF SEQ ID NOS: 65;
SOFTWARE: FastSRQ for Windows Version 4.0;
SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                                             Length 449;
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                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
FORMATION: A polypeptide encoded by SEQ ID NO:7.
US-09-843-250-18
                                                                                                                                                                                                                                                                                                                                                         Query Match 97.4%; Score 2346; DB 11;
Best Local Similarity 96.7%; Pred. No. 6.9e-220;
Matches 434; Conservative 10; Mismatches 5;
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                                                   CURRENT FILING DATE: 2001-04-26
REIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR PLING DATE: 1999-10-26
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 449
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                                     CURRENT APPLICATION NUMBER: US/09/843,250
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                      Sequence 17, Application US/09843250
Publication No. US2003002233541
GENERAL INFORMATION:
APPLICANT: Parales R.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
ITILE OF INVENTION: NO. US20030022335Alel naphthalene dioxygenase and methods for the TILE REFERENCE: 875.005402
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT PILING DATE: 2001-04-26
PRIOR PILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
SEQ ID NO 17
IENGTH: 449
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Publication No. US20030022335A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resmick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
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99.4%; Score 2394; DB 11; Length 449;
Best Local Similarity 99.3%; Pred. No. 1.4e-224;
Matches 446; Conservative 1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:6.
US-09-843-250-17
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181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 OMISKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQBRINKEIGDVRARIYRSHLMCTV 300
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                                                                                                                                                                                                                    1 MAYNAKILVSESCLSOKHLIHGDEELPOHELKTIFARNAFLTHDSLIPARGDYVTAKAG 60
                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                      Query Match
Best Local Similarity 95.5%; Pred. No. 3.7e-217;
Matches 429; Conservative 12; Mismatches 8; Indels 0
                                             FRATURE:
CTHER INFORMATION: A polypeptide encoded by SEQ ID NO:8.
NAME/KEY: SITE
LOCATION: (35)...(35)
OTHER INFORMATION: Xaa = any amino acid.
US-09-843-250-19
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               TYPE: PRT ORGANISM: Artificial Sequence
LENGTH: 449
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Search completed: December 9, 2003, 16:09:34 Job time: 23:1429 sece

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 9, 2003, 15:44:13.; Search time 11.8571 Seconds (without alignments) 1602.205 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-843-250-2
2408
1 MNYNNKILVSESGLSQKHLI.....AEFBHASSTWHTELFKTTDR 449

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched:

328717 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

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6: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

		*			SUMMARIES	
Result No.	Score	Query	Length DB	DB	ID	Description
-	408.5	17.0	463	4	IIS-09-252-9918-31267	
8	407.5	16.9	496	. 4	TIS-09-328-352-6452	
m	388	16.1	445	٠ ٦	TIR-00-308-0408	Sequence 5452, Ap
4	388	16.01	777	۲ ٦	110-00-020-000-1248	
	354		110	۴ <	110 00 100 110 110 110 110 110 110 110	31385,
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۰ ۰	2000	14.5	4.0	4.	US-US-252-991A-17164	
0 0	0 0 0	9.14	375	4	US-09-328-352-4700	•
7	637.5		529	4	US-09-252-991A-19627	
O :	224	6	446	4"	US-09-004-393B-4	
11	223	6.9	439	₹*	US-09-004-393B-2	Segience 2, Appli
12	185	7.7	35	m	US-08-810-009-19	
13	174	7.2	35	m	US-08-810-009-20	ic
14	168	7.0	35	m	US-08-810-009-21	
15	143.5	6.0	629	4	US-09-252-991A-27100	,,,,,
16	128	5.3	392	4	US-09-328-352-6765	
17	118.5	4.9	354	4	US-08-976-063R-4	
18	112.5		379	٠,	US-09-028-34	Sequence 4, Appril
19	110	4.6	35	m	US-08-810-009-12	Sequence 36, Appl
20	109		35	m	US-08-810-009-14	Semience 12, Appl
21	109	4.5	622	4	US-09-311-626B-4	Ϊ,
22	108	4.5	50	(1)	US-08-810-009-13	- :
23	108	4.5	er er	~	135-08-810-009-15	
24	106	4.	, c	• ~	0-000-010-00-	Sequence 15, Appl
25	106	4	790	, ,	100 OCC 00 000	
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Sequence 16, Appl	16	Sequence 16, Appl	Sequence 15, Appl Sequence 15, Appl	Sequence 15, Appl	Seguence 15, Appl	Sequence 11. Appl		Sequence 10, Appl	44	Sequence 45, Appl	5961	Sequence 17, Appl	57.	466.	2837	Sequence 46, Appl
US-09-689-914A-16	US-US-689-913A-16	110-03-606-30-15 110-08-606-30-15	US-09-689-914A-15	US-09-689-913A-15	US-09-689-916A-15	US-08-810-009-11	US-08-810-009-8	US-08-810-009-10	US-08-810-009-44	US-08-810-009-45	US-09-328-352-5961	US-08-810-009-17	US-09-325-932A-57	US-09-198-452A-466	US-09-252-991A-28371	US-08-810-009-46
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103.5	103.0	103.5	103.5	103.5	103.5	103	102	102	101	101	100.5	100	99.5	66	97.5	92
28	7 C	9 -	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

SULT 1 -09-252-91A-31367 Sequence 31357, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION: APPLICATION: APPLICATION: APPLICATION NUMBER: US/09/252,991A TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS CURRENT FILLE OF INVENTION NUMBER: US/09/252,991A CURRENT FILLING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR FILING DATE: 1998-07-27 WUMBER OF SEQ ID NOS: 33142 SEQ ID NO 31367 LENGHYH; 463 TTYPE: PRT ORGANISM: Pseudomonas aeruginosa -09-252-991A-31367	Query Match 17.0%; Score 408.5; DB 4; Length 463; Best Local Similarity 29.0%; Pred. No. 1.4e-30; Matches 110; Conservative 69; Mismatches 149; Indels 51; Gaps 17;	23 DEBLPQHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDBVIVSRQNDGSIRAFLNVCR 82 : :	83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKE 137 	138 VARVESFHGFIYGCFDQBAPPLADYLGDAAWYLBPMFKHS-GGLELVGPPGKVVIKANWK 196 	197 APAKNFVGDAYHVGWTHASSIRSGESIFSSLAGNAALPPEGAGLQ 241 	242 MTSKYGSGMGVLMDGYSGVHSADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCT 299 1	300 VFPNNSML-TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGFAGFW 358
RESULT 1 US-09-252-991A-31367 Sequence 31367, Applicant No. 6551795 GENERAL INFORMATION APPLICANT: TITLE OF INVENTION TITLE OF INVENTION FILE OF SECOND FRICK FILE OF SECON	Query Match Best Local Matches 11	2 04 05	9 24	Oy 13	Qy 19 Db 21	Qy 242 Db 266	Oy 30 Db 31
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APPLICANT: MAIC O' Rubenfield et al.
APPLICANT: MAIC O' Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-02-18
PRIOR PLING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31385
LENGTH: 466
                                                                                                                                                                                                                         193 ANWKAPABNFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLQMTSKYGS 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           294 ---SHINCTVFPNNSMLTCS-GVFKVWNPIDANTTRVWTYAIVEKD----MPEDLKRRLA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 VGGSGFNINLFPN---IACSMAFFRVIQPISVAETEI-HHSVITWDGGPQIANQYRLRIH 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 EHFQ---GPFGFGTPDDSEAMERV-QHGAN-AGNDLMIMINRGL------PGEVKT 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 PAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMT---SKYGSGMGVL- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                          80 VCRHRGKTLVSVEAGNAKGFVCSYHGFGSNGELQSVPPEKDLYGESLNKKCLGLKEVA
                                                                                                                                                                                              140 RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGG--LELVGP-----PGKVVIK
                                                                                                                                                                                                                                                                                                                                  ------FEN
                                                                                                                                                                                                                                                                                                                                                                      249 GMGVLWDGYSGVHSADLVPBLMAFGGAKOER-LNKEIGDVR------ARIYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVQRTVGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVG-
                             IHGDEELPQHELKTI PARNWLPLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV -- PPEKDLYGESLNXKCLGLKEVAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 DEBLECHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDBVIVSRQNDGSIRAFINVCR
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                                                                                                                                                                                                                                                                                                                             220 -NWKIQLEN-TTDAYHFPLVHKSFLSSVDEKTERLFN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31385, Application US/09252991A Patent No. 6551795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 EDGLKSDVSAETGMRAAYOOWK 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31385
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                                                                                                                                        Sequence 6452, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7248, Application US/09328352

Patent No. 6562958

GRINERAL INFORMATION: •

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER FILE REFERENCE: GYC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENFVGDAYHVG---WIHASSLRSGESIFSSLAGNAALPPEGA-GLOMISKYG--SGMGVI, 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR--IYRSHLNCTVFPNNSMLTCSG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 DEBLFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 31.3%; Pred. No. 2e-30;
Matches 105; Conservative 59; Mismatches 146; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
16.1%; Score 388; DB 4; Length 445;
Best Local Similarity 28.1%; Pred. No. 1.2e-28;
Matches 124; Conservative 66; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        312 -VPKVMNPIDANTTEVWTYALVEK-DMPEDLKRRL 344
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                        374 TPDDLEBFRSCQQG---YQ 389
359 ESDDNDNMETASQNGKKYQ 377
                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 445
; TYPE: PRT
; ORGANISM: Actinetobacter baumannil
US-09-328-352-7248
                                                                                                      RESULT 2
US-09-328-352-6452
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US-09-328-352-7248
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Sequence 25088, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGANOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: ARROGANOSA FOR DIAGNOSTICS AND THERAPBUTICS
TITLE OF INVENTION: ARROGANOSA FOR DIAGNOSTICS AND THERAPBUTICS
TILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR PILING DATE: 1999-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR PLING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO SEQ BD NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.5%; Score 348.5; DB 4; Best Local Similarity 27.4%; Pred. No. 6.9e-25; Matches 114; Conservative 72; Mismatches 177;
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                                                                                                    JS-09-252-991A-25088
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Sequence 7581, Application US/09328352
Patent No. 6562958
GENERAL INCOMPATION.
FAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7581
LENGTH: 471
AGFWESDDNDWETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYR 414
                                                                                           -----ADLVPELMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                                                                --- BYGQARAEWMHRL 315
                                                                                                                                                                                                         -NCIVPPNNSML-TCSGVFKVMNPIDANTTBVWTYAIVEKDMPEDLKRRLADSVQRTVGP 354
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                                                                                                                                 267 DGWFSFANGHSVLFSEMPNPAVRPGYASVMPRLVA----
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US-09-328-352-7581
                                                                                              ---MDGYSGVHS---
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US-09-328-352-7581
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Best Local S
Matches 114
                                                                                           254
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53; Gaps

Indels

84 84 201 201

APPLICANT: MAIC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PLILOM INVERE: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142 246 247 SGPPSTGRPIAYWSPLFPRALKPSIAAKFRRLVBRFGQARAEDIAHTWKSLFIFPNLVIN 306 S-----ADLVPB-IMAFGGAKOERLNKEIGDVRAR-IYRSHLNCTVFPN---N 304 307 DILGEN-IRSFFPTAADEVSVTVWGAGFADETREERAARINGLISFIGPGGFGTPDDVE 364 305 SMLICSGVFKVMNPIDANITEVMTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWESDDND 364 202 GV-DAYHLPPAHKRYLBYLNTL------GTDPESHKRHGRG-EALGNGHALII 365 NMBTASONGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 365 ILESCQ---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREH 407

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Sequence 19627, Application US/09252991A

Sequence 19627, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 107196, 136

CURRENT PILLING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

RECORD APPLICATION NUMBER: US 60/094,190

NUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
                           232 TTHQNWTLQYG------FARSSEKSFKLDPSVTDPEFHGEWT-WPCTMFNVPPGSN 280
                                                                                                                                                                                                   191 IK--ANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90 SVEAGNAKGFVCSYHGWGFGSNGELQSVPPEKDLYGESLNKKC-LGLKEVARVESFHGFI 148
                                                                                                                                                                             ---EKOM-----PEDLKRRLADS 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149 YGCFDQEAPPLADYLGDAAWYLEPMFKHSGGLB.-LVGPPGKVVIKANWKAPAENFVGDA 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344 NHVPFVHPKTFLPVMTAPVRGLAREAAVPSBVLRLLQEGETPELRSLSFPTKAPIQPYKS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249 GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLT 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 QIECTGQRPLVCPYHAWSFGAEGLQGIP-NSSLYQFSAEERARIGLRKL-HLEEVGGLJ
                                                                                       249 GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVF---PNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 ELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.9%; Score 237.5; DB 4; Length ! 24.9%; Pred. No. 4e-14; ive 54; Mismatches 139; Indels
                                                                                                                                                                             306 MLTCSGVFKVWNPIDANTTEVWTYAIV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09004393B; Patent No. 6310271; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.99
Matches 86; Conservative
                                                                                                                                                                                                                                                              348 VORTVGPAGF 357
                                                                                                                                                                                                                                                                                                    334 VORGLKSRGY 343
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US-09-004-393B-4
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Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT APPLICATION DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4700
                                                                                                                                                                                                                                            HRGKTLVSVBAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                             257 YSGVHSADLVPELMA-FG---------GAKQ---ERLNKEIGDVRA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIK-----ANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                197 APAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGYLWDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227 LVIEN-NRECYHCNGSHPELLK-----TLLEWDDVTDPRAS--QAFKDQVAACTSAWD- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         290 RIYRSHINCTVFFNNSMLTCSG----VFKVWNPIDANTTEVWTYALVEKDMPE---- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----DEKRRLADSVQRTVGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNIG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 RLREVWDATNDQDRRLAEENQRGINSDAYQPGPYSKTYEFGVINFLDWYS--ERMLANLG 437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131 KCLGLKEVARVESFHGFIYGCFDQBAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
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                                                                                                                                                                                                                 23 DEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLMVCR
                                                                                                                                                                             Gaps
                                                                                                                                                                        96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  th 11.6%; Score 280.5; DB 4; Length 375; Similarity 26.2%; Pred. No. 1.8e-18; 97; Conservative 58; Mismatches 130; Indels 85
                                                                                                                                  Length 449;
                                                                                                                              i; Score 295; DB 4; Length 449;
i; Pred. No. 9.8e-20;
54; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 375
TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17164
                                                                                                                         Query Match
Best Local Similarity 26.4%;
Matches 111; Conservative 5
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Matches 97; Conserv
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SEQ ID NO 17164
                    LENGTH: 449
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224 FVLISLDRSLEEGGDVGTEWLGTSA---BDVKAHAFDPSLQFI-HRSEFPWESNWKIPSD 279
                              147 FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                    Sequence 19, Application US/08810009
Patent No. 611437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS;
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEB: BELL, SELTZER, PARK & GIBSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20, Application US/08810009
; Patent No. 6211437
; GENERAL INFORMATION:
    APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Johal, Gurmukh S. TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
    TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%; Score 185; DB 3; Length 35; Best Local Similarity 94.3%; Pred. No. 6.6e-11; Matches 33; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TO SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR.1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPHONE: 919-881-3175
                                                                                                                        201 NPVGDAYHVGWTH 213
                                                                                                                                                                        280 NYLDSSYHVPYAH 292
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-810-009-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 DGSIRAFLINYCRHRGKTLVSVEAGNAKGFYÇSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMD----YLGDA-----AWYLEPMFKHSGGLE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87 TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        167 SILACGSGKKSCFVCPYHGWYYGWDGSLAKASKAKP--BQNLDPKBLGLVPL-KVAVWGP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 BSGLSOKHLIHGDEELFQHELKTIFARNWIFLTHDSLIPAPGDYVTAKMGIDEVIVSRON 70
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                    APPLICANT: Rathinasabapathi, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
FILE REFERENCE: UP-162
CURRENT APPLICATION WHBER: US/09/004,393B
PRIOR APPLICATION WHBER: G0/035,147
PRIOR FILING DATE: 1997-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09004393B
Patent No. 6310271
GENERAL INFORMATION.
APPLICANT: Hanson D., Andrew
APPLICANT: Rathinsabapathi, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polymotleotides Encoding Choline Monooxygenase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
9.3%; Score 223; DB 4; Length 439;
Best Local Similarity 30.1%; Pred. No. 7.3e-13;
Matches 58; Conservative 38; Mismatches 83; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.3%; Score 224; DB 4; Length 446;
Best Local Similarity 27.4%; Pred. No. 6e-13;
Matches 58; Conservative 37; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 F-----PMECNWKVFCDNYLDSSYHVPYAH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 LVGPPGKVVIKANWKAPABNFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: UF-16.
CURRENT APPLICATION NUMBER: US/09/004,393B
CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/035,147
PRIOR FILING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
Hanson D., Andrew
                                                                                                                                                                                                                                                           Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Spinacia oleracea
US-09-004-393B-2
                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-004-393B-4
                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ve
SEQ ID NO 4
LENGTH: 446
APPLICANT:
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Gaps

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Search completed: December 9, 2003, 15:45:52 Job time : 13 secs
                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-81-3140
TELEFAX: 919-81-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas aeruginosa
                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                            ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-810-009-21
                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS:
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; Sequence 21, Application US/08810009
; Ratent No. 6211437
; GENERAL INFORMATION:
APPLICANT: Briggs Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
ITILE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
CORRESPONDENCE ADDRESS:
ADDRESSER: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 174; DB 3; Length 35; Best Local Similarity 85.7%; Pred. No. 7.4e-10; Matches 30; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIPICATION: 800
ATTONREY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPAK: 919-881-3175
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-WAR-1997
CLASSIPICATION: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 NVCRHRGKTLVNARAGNAKGPVCGYHGWGFGSNGK 35
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Flopby disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPAX: 919-8813175
TELEX: 575102
INPORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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US-08-810-009-21
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APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27100
LENGTH: 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 P-------GQRVRGFPCIRRFPVQERHGFVWVWPGAEEQADAALIPRL---EWAESP 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 NWKILVSESGLSQKHLI--HGDEELFQHELKTIFARN--WLFLTHDSLIPAPGDYVTAKM 59
                                                               Gaps
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      Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 MPKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSL----
                                                                                                                  79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                 1 NVCRHRGKTIVDAEAGNAKGPVCGYHGWGYGSNGK 35
Query Match
7.0%; Score 168; DB 3;
Best Local Similarity 80.0%; Pred. No. 2.8e-09;
Matches 28; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 SGESIFSSLAGNAALPP-----EGAGL 240
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                                                                                                                                                                                                                                                                                                              Sequence 27100, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
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Sequence 6452, Ap sequence 31367, A Sequence 31385, A Sequence 7581, Ap Sequence 7581, Ap Sequence 17164, Applisequence 2, Applisequence 2, Applisequence 21, Applisequence 21, Applisequence 4, Applisequence 14, Applisequence 14, Applisequence 14, Applisequence 14, Applisequence 14, Applisequence 15, Applisequence 16, Applisequence 16,
                                                                                                                                                                                             December 9, 2003, 15:44:13; Search time 11.8571 Seconds (without alignments) 1602.205 Million cell updates/sec
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2410
1 MNYNNKILVSESGLSQXHLI.....AEFEHASSTWHTELTKTTDR 449
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-252-911A-31367
US-09-252-911A-31367
US-09-252-911A-31385
US-09-252-991A-7148
US-09-252-991A-7164
US-09-252-991A-7164
US-09-252-991A-1764
US-09-252-991A-1764
US-09-252-991A-1764
US-09-004-393B-2
US-09-004-393B-2
US-08-810-009-21
US-08-810-009-21
US-09-328-352-675
US-09-328-352-675
US-08-810-009-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length
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Perfect score:
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Sequence 16, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 15, Appl Sequence 18, Appl Sequence 18, Appl Sequence 10, Appl Sequence 44, Appl Sequence 44, Appl Sequence 46, Appl Sequence 46, Appl Sequence 57, Appl Sequence 57, Appl Sequence 66, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl		RNCES RELATING TO ACINETOBACTE	Length 496; Indels 25; Gaps 13;	TVSRQNDGSIRAFLNVCR 82 :: : : IARNRNGELNAMINACS 132	XGESLNKK-CLGLKBVAR 140 : : :XSDCFNQDGSHDLKKVAR 192	LVGPPGKVVIKANWKAPA 199 ::	FSSLAGNAALPPEGA-GLOMTSKYGSGMGVL 253 :	SHINCTVFPNNSMLTCSG 311 :: :: SR-NLCLYPNVYLMDQFG 360	
4 US-09-689-913A-16 4 US-09-689-916A-15 3 US-08-689-916A-15 4 US-09-689-916A-15 4 US-09-689-916A-15 4 US-09-689-916A-15 3 US-08-810-009-11 3 US-08-810-009-44 3 US-08-810-009-44 3 US-08-810-009-44 3 US-08-810-009-44 3 US-08-810-009-44 4 US-09-328-352-5961 4 US-09-328-352-5961 5 US-09-328-352-5961 6 US-09-328-352-5961 7 US-09-328-352-5961 8 US-08-811-009-17 9 US-09-328-352-5961 9 US-09-188-452A-466 1 US-09-188-528-57	ALIGNMENTS	S/09328352 tr al. ACID AND AMINO ACID SEQUENCES RELA II FOR DIAGNOSTICS AND THERAPEUTICS US/09/328,352 6-04	Score 407.5; DB 4; Pred. No. 3.8e-31; 59; Mismatches 146;	DEBLFQHELKTIFARNWLFLTHDSLIPAPGDXVTAROMGIDEVIVSRQNDGSIRAFLNVCR 	HRGKTLVSVBAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKK-CLGLKEVAR 	VESEHGRIYGCFDQRAPPIMDYLGDAAWYLEPWFKHS-GGLELVGPPGKVVIKANWKAPA : : : : :	RNFVGDAYHVGWTHASSLRSGBSIFSSLAGNAALPPEGA-GLOMTSKYG	#DGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVFPNNSMLTCSG :-	-VFKUWNPIDANTTEVWTYALVEK-DMPEDLKRRL 344
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		ESULT 1 S-09-328-352-6452 Sequence 6452, Application US/09328352 Patent No. 6562958 GENERAL INFORMATION: APPLICANT: GATY, Breton et al. TITLE OF INVENTION: NUCLEIC ACID AND TITLE OF INVENTION: BADWANNII FOR DIA FILE REFERENCE: GTC99-03P4 CURRENT APPLICATION NUMBER: US/09/328 CURRENT FILING DATE: 1999-06-04 NUMBER OF SEQ ID NOS: 8252 LENGTH: 496 TYPE: RFT ORGANISM: Acinetobacter baumannii S-09-328-352-6452	16.9%; Similarity 31.3%; 5, Conservative	BELPQHELKTIFARN BALPDLEMKYIFEGN	rgktlvsveagnakg 	VESFHGFIYGCFDQEA : :: FESYKGFLFGSLNPDV	ENFVGDAYHVGWTHASSLRSGESI 	WDGYSGVHSADLVPEL :: WTQWANPEDRPNFP	VFKVWNPIDANTTEV
105.5 105.5 105.5 105.5 105.5 100.5		ULT 1 09-328-352-6 equance 6452 atent No. 65 atent No. 65 atent No. 67 atent No. 7 atent No. 67 atent No. 645 atent No. 64	55.5	23 D 73 D	83 H	141 V 193 F	200 E 253 E	254 W	312 -
00000000000000000000000000000000000000		RESULT 1 US-09-328-352-6452 ; Sequence 6452, A ; Patent No. 65629 ; GENERAL INFORMAT ; APPLICANT; GALY ; TITLE OF INVENT ; CURRENT APPLICAT ;	Query Ma Best Loc Matches	& 8	ඊ සි	& A	දු දු	& A	& 8
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RESULT 2 US-09-252-991A-31367 ; Sequence 31367, Application US/09252991A

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Sequence 31355, Application US/09252991A
Fadent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc O' Rubenfield et al.
APPLICANTON NUMBER: US O' DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 101196,133
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR PILING DATE: 1999-02-18
FRIOR FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-07-13
FRIOR FILING DATE: 1998-07-13
FRIOR FILING DATE: 1998-07-13
FRIOR FILING DATE: 1998-07-17
FRIOR DATE: 1998-07-17
FRIOR FILING DATE: 1998-07-17
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                                            193 ANWKAPAENFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLOMTSKYGS
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                   IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
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16.0%; Score 384.5; DB 4; Length 466;
Best Local Similarity 27.3%; Pred. No. 6e-29;
Matches 122; Conservative 76; Mismatches 176; Indels 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 -NWKIQLEN-TTDAYHFPLVHKSFLSSVDEKTEELFN----
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Ratent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUDANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: US/09-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PELING DATE: 1999-06-04
SEQ ID NO 7248
GENERAL INFORMATION:
APPLICANT:
MARC J. RUBERICA CLD AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPRUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/0742, 991A
CURRENT PILING DATE: 1999-02-18
FRIOR PILING DATE: 1999-02-18
FRIOR PLILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31367
LENGTH: 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV--PFEKDLYGESLNKKCLG---LKE 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 16.9%; Score 406.5; DB 4; Length 463; Best Local Similarity 29.0%; Pred. No. 4.2e-31; Matches 110; Conservative 69; Mismatches 149; Indels 51
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16.1%; Score 388; DB 4; Length 445;
Best Local Similarity 28.1%; Pred. No. 2.5e-29;
Matches 124; Conservative 66; Mismatches 164; Indels
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US-09-328-352-7248
                                                                                                                                                                                                                                                                                                                                                                Pseudomonas aeruginosa
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US-09-328-352-7248
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GENERAL INPORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                  CURENT APPLICATION WHERE: US/09/252,991A
CURENT FILING DATE: 1999-02-18
CURENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

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                                                                                     RESULT 6
US-09-252-991A-25088
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Patent No. 6562958
GRNERAL INFORMATION:
APPLICANT: Gary L. Barton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPRESENCE: GTO99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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267 DGWFSFANGHSVLFSEMPNPAVRPGYASVMPRLVA------EYGQARAEMMMHRL 315
                                                                                                                                                                                                                                                         297 -NCTVPPNNSML-TCSGVPKVMNPIDANTTEVMTYAI-VEKDMPEDLKRRLAD----SV 348
                                                                                                                                                                                                                                                                                                      316 RNIALYPSIEVIDQISSQLRIVRPLAWNRTEIVSQCIGVKGESDADRENRIRQFEDFFNV 375
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                                                                                                               254 --WDGYSGVHS------ADLVPBLMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                                                                                                                                                                                                                                                                                                   349 QRIGGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAI 408
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US-09-328-352-7581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.34
Matches 112; Conservative
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US-09-328-352-7581
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LENGTH: 471
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GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-27
NUMBER OF SEQ ID NOS: 33142
                                                                                               15:
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                                                                                                                                                                                                                                                                                                                                                                                                  85 GAKVCAERQGNSQRFTCPYHGWTYDSHGSLIGLP-DKAAYQHA--GQCHPELSLTRVKHA 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 VYRNFLFIHYAARQPSLETXLGQAKDYIDLICDQSBABLEIIPGGFEHSIKANWKLLAEN 201
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                                                                                                                                                                                                                                   25 ELHRRELHEIFDDSWLYAAHLSELREPGDFITRDVGGRNLIIQRRADGEPAVYLNACAHR
                                                                                                                                                                        25 BIPOHELKTIFARNHIFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCRHR
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                                                                                               53; Gaps
Query Match 14.2%; Score 341.5; DB 4; Length 425; Best Local Similarity 27.4%; Pred. No. 8.2e-25; Matches 114; Conservative 71; Mismatches 178; Indels 53
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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
MAY OF INVENITON:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENITON:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENITON:
NUCLEIC APPLICATION
NUMBER: US 09/252,991A
CURRENT APPLICATION
NUMBER: US 00/074,788
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEG ID NO 19627
                                                                                                                                                                                 232 TTHQNWTLQYG------FARSSEKSFKLDPSVTDPEFHGFWT-WPCTMFNVPPGSN 280
             131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVV 190
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                                    : | | : | : | : | : | : | 141 SMVPLK----VEEYAGFVFINMDENATCVEDQL---PGFAERINQACGVIKULAARFV
                                                                                   191 IK--ANWKAPABNFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS
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| CTECTGQRPLVCPYHAMSFGAEGQLQGIP-NSSLYQFSAEERARIGLRKL-HLEEVGOLL
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9.9%; Score 237.5; DB 4; Length 5
Best Local Similarity 24.9%; Pred. No. 1.6e-14;
Matches 86; Conservative 54; Mismatches 139; Indels
                                                                                                          #04 WFSDLCEGYGDEH-------
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US-09-252-991A-19627
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US-09-252-991A-19627
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Patent No. 6562958
Patent No. 6562958
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4700
LENGTH: 375
                                                                                                                                                                                                          HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                227 IVIEN-NRECYHCNGSHPEILK-----TLLEWDDVTDPRAS--QAFKDQVACTSAWD- 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               380 RLRE------VWDATNDQDRRIAEENQRGINS-------DAXQPGPYSK 415
                                                                                                                                                                                                                                                                                                                                SFHGFIXGCFDQBAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIK-----ANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                      197 APAENFVGDAXHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLOMTSKYGSGMGVLWDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ABKIPYAHASFGLRNRIVRMPLLDGTVSMTMDGKQGSKKIMGRIKNPDLGSMRI 330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----IHL-----PHSWNHCMGDHLIVFTVW-PISAQETLVTTKWLVHKDAVEGVDYDVA 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 DSVQRTGGPAGFWESDDNDNWETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGK 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVCRHRGKTLVSVEAGNAKGFV-CSYHCWGFGSNGELQSV-----PFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
                                                                                                                                                                                 23 DEBLPOHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDBVIVSRONDGSIRAFLNVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 LIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFL
                                                                                                              ; Score 291; DB 4; Length 449;
; Pred. No. 7.6e-20;
61; Mismatches 161; Indels 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.5%; Score 276.5; DB 4; Length 375;
Best Local Similarity 26.4%; Pred. No. 1.5e-18;
Matches 96; Conservative 56; Mismatches 126; Indels 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT; ORGANISM: Acinetobacter baumannii US-09-328-352-4700
; SEQ ID NO 17164
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Reeudomonas aeruginosa
US-09-252-991A-17164
                                                                                                              12.14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     406 S-AIGETSYRGFY 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 TYEFGVINFLDWY 428
                                                                                                        Query Match
Best Local Similarity 25.24
Matches 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-328-352-4700
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APPLICANT: Briggs, Steven P.
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                                        GENERAL INFORMATION.

APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Rathinasabapathi, Bala
TITLE OF INVENTION: Polymucleotides Encoding Choline Monooxygenase and
FILE REFERENCE: UP-162
CURRENT FILING DATE: 1998-01-08
FRIOR PELING DATE: 1997-01-08
FRIOR FILING DATE: 1997-01-08
FRIOR FILING DATE: 1997-01-08
FRIOR PELING PARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: Hanson D., Andrew
APPLICANT: Rathinsachapathi, Bala
APPLICANT: Rathinsachapathi, Bala
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
FILE REFERENCE: UP-162
CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/035,147
PRIOR APPLICATION NUMBER: 60/035,147
PRIOR PLING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 6
SOFTHARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 BDALRPPSTWYTRPAFYSHELBRIFYKGWQVAGYSEQVKEKNQYFTGSLGAVUBYLVSRDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 DGSIRAFLAVCRHRGKTLVSVEAGNAKGFYCSYHGWGFGSNGELQSVPFFKDLYGESLAK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMD----YLGDA----AWYLEPMFKHSGGLE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 BSGLSOKHLIHGDEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 POHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCRHRGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
9.3%; Score 224; DB 4; Length 446;
Best Local Similarity 27.4%; Pred. No. 2.6e-13;
Matches 58; Conservative 37; Mismatches 97; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.3%; Score 223; DB 4; Length 439; 30.1%; Pred. No. 3.2e-13; tive 38; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 F-----PMECNWKVPCDNYLDSSYHVPYAH 299
Sequence 4, Application US/09004393B Patent No. 6310271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09004393B Patent No. 6310271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Spinacia oleracea
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Best Local Similarity 30.11
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-004-393B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-004-393B-2
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                                  167 SILACGSGKKSCFVCPYHGWVYGMDGSLAKASKAKP--EQNLDPKELGLVPL-KVAVWGP 223
                                                                                                        147 FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                             224 FVLISLDRSLEBGGDVGTEWLGTSA---EDVKAHAFDPSLQPI-HRSEFPWESNWKIFSD 279
87 ILVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTINUATION TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: TIBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATONENEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 5718-4
TELEPHONE: 919-881-3175
TELEBRAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.7%; Score 185; DB 3; I Best Local Similarity 94.3%; Pred. No. 3.3e-11; Matches 33; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08810009
Patent No. 6211437
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Patent No. 6211437
GENERAL INFORMATION:
                                                                                                                                                                                                                                                            280 NYLDSSYHVPYAH 292
                                                                                                                                                                                                                      201 NFVGDAYHVGWTH 213
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-19
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459 GDEVITSRHMQNVMAPPFFWRMALRGNGL 486
                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPHONE: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE; PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27100
                                                                                                                                                                                                                                         21:
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.0%;
Best Local Similarity 80.0%;
Matches 28; Conservative
                                                                                                                                                                                                                                                                              LENGTH: 35 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                              TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-810-009-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 65; Conserva
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APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSES: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 21, Application US/08810009
| Patent No. 6211437
| GENERAL INFORMATION: BELGSS, Steven P. APPLICANT: Briggs, Steven P. APPLICANT: Johal, Gurmukh S. APPLICANT: Johal, Gray, John TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING TITLE OF INVENTION: GELL DEATH AND DISEASE RESISTANCE IN PLANTS (CORRESPONDENCE ADDRESSE BELL, SELITZER, PARK & GIBSON STREET: P.O. Drawer 34009 CITY: Charlotte
| CONTRY: Charlotte CONTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.2%; Score 174; DB 3; Length 35; Best Local Similarity 85.7%; Pred, No. 3,9e-10; Matches 30; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPTARE: BACENTIN Release #1.0, Version #1.30
SOUTHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR.1997
CLASS: FICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Sprinll, W MAYRAY
REGISTRATION NUMBER: 5718-4
TELEPHONE: 919-881-3175
ITELEPHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHRARATERSTICS:
LEMETH: 35 antio acids
FARMATHER STREET COMPATION FOR SEQ ID NO: 20:
SEQUENCE CHRARACTERISTICS:
LEMETH: 35 antio acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparatible
COMPUTER: Floppy disk
COMPUTER: For Comparatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 NVCRHRGKTLVSVBAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / MOLECULE TYPE: protein
US-08-810-009-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-810-009-21
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PARENEL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEEC ACID AND THERAPEUTICS

TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27100

LENGTH: 629
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       Length 35;
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                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                      79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
Score 168; DB 3;
Pred. No. 1.5e-09;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-27100
; Sequence 27100, Application US/09252991A
; Patent No. 6551795
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Search completed: December 9, 2003, 15:45:53 Job time : 13 secs

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December 9, 2003, 15:44:14; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec
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2410
1 MNYNNKILVSESGLSQKHLI......AEFEHASSTWHTELTKITDR 449
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| cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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| cgn2_6/ptodata/1/pubpaa/NS07_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/prodata/1/pubpaa/USO3_NEW_PUB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            684280 seqs, 185983659 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMEDIES

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		Appl	Appl	Appl	Appl	Appli	Appl	App1								
		32,	33.	34.	28	7	14.	12,	26,	59	32,	36,	16,	17.	18,	19
	Description	Sequence	Segmence	Sequence	Sequence	Segmence	Sequence	Seguence	Sequence	Sequence	Sequence	Seguence	Seguence	Segmence	Sequence	Sequence
SUMMARIES	ΩΙ	US-09-843-250-32	US-09-843-250-33	US-09-843-250-34	US-09-843-250-58	US-09-843-250-2	US-09-843-250-14	US-09-843-250-15	US-09-843-250-26	US-09-843-250-59	US-09-843-250-35	US-09-843-250-36	US-09-843-250-16	US-09-843-250-17	US-09-843-250-18	US-09-843-250-19
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	Query Match Length DB	449	449	449	449	449	449	449	449	449	449	449	449	449	449	449
de	Ouery Match	100.0	8.66	7.66	99.7	99.6	99.6	99.6	99.6	9.66	9.66	99.6	99.4	99.2	97.2	96.1
	Score	2410	2404	2402	2402	2401	2401	2401	2401	2401	2400	2400	2396	2391	2343	2315
	Result No.	н	Ņ	m	4	co	w	7	∞	O	10	11	. 12	13	14	15

	7	Sequence 21, Appl	22	23,		Sequence 10253, A	Sequence 11692, A		Sequence 5097, Ap	•	9		Sequence 20, Appl	20,	21,	7	4,	12	Sequence 12, Appl	14	14,	13,	15,	13,	15,	Sequence 4, Appli	8	9, A	9, Ag	a
00 000 000 000	11 US-03-843-80-80 TT	11 US-09-843-250-21	11 US-09-843-250-22	11 US-09-843-250-23	11 US-09-843-250-24	9 US-09-815-242-10253	9 US-09-815-242-11692	10 US-09-738-626-6140	9 US-09-815-242-5097	15 US-10-156-761-14477	9 US-09-776-490-19	9 US-09-776-491-19	9 US-09-776-490-20	9 US-09-776-491-20	9 US-09-776-490-21	9 US-09-776-491-21	8 US-08-976-063C-4	9 US-09-776-490-12	9 US-09-776-491-12	9 US-09-776-490-14	9 US-09-776-491-14	9 US-09-776-490-13	9 US-09-776-490-15	9 US-09-776-491-13	9 US-09-776-491-15	15 US-10-124-880-4	14 US-10-047-542-78		9 US-09-776-491-9	10 US-09-924-097-15
•	4	449	447	447	451	453	385	490	424	382	35	32	35	32	35	32	354	35	35	32	35	35	35	35	35	622	548	35	35	951
L	35.0	92.0	90.7	85.0	81.6	30.5	15.7	15.6	13.8	10.3	7.7	7 7	7.2	7.2	7.0	7.0	4.9	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5	4.5	5.5	4.4	4	4.3
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ALIGNMENTS

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Sequence 32, Application US/09843250;
Fublication No. US2003022335A1
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE OF INVENTION NUMBER: DS/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCI/US99/10-26
PRIOR APPLICATION NUMBER: W $60/105,575
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IDBVIVSRQNDGSIRAFLNVCRHRGKTLVSVRAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:27.
US-09-843-250-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 449; Conservative
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QY 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 Db 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 QY 301 FPNNSMLTCSGVFKVMNPIDANTTEVMTYAIVEKDMFEDLKRRLADSVQRTGGPAGFWES 360 Db 301 FPNNSMLTCSGVFKVMNPIDANTTEVWTYAIVEKDMFEDLKRRLADSVQRTGGPAGFWES 360 QY 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QY 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QY 421 QMTSSSNNAEFEHASSTWHTELTKTTDR 449 Db 421 QMTSSSNNAEFEHASSTWHTELTKTTDR 449	RESULT 3 US-09-843-250-34 i Sequence 34, Application US/09843250 j Sequence 34, Application WS/09843250 j GENERAL INFORMATION: APPLICANT: Parales, R. APPLICANT: Parales, R. APPLICANT: Resulck, S.	. US200: 6482 MBER: U 2001-04 2001-04 210-26 ER: US (55 110-26 61ndows 41ndows	Query Match 99.7%; Score 2402; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 2.8e-226; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY 1 MNYNNKILVSESGLSQKHLIHGDBELFQHBLKTIFARNWLFLTHDSLIPAPGDYVTAKNG 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 61 IDEVIVSRQNDGSIRAFLAVCRHRGKTLVSVBAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 Db 61 IDEVIVSRQNDGSIRAFLAVCRHRGKTLVSVBAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 Qy 121 KDLYGESLINKKCLGLKEVARVBSFHGFIYGGFDQBAPPLMDYLGDAAWYLEPMFKHSGGL 180 Db 121 KDLYGESLINKKCLGLKEVARVESFHGFIYGGFDQBAPPLMDYLGDAAWYLEPMFKHSGGL 180	QY 181 ELVGPPGKTVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 Db 181 ELVGPPGKTVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 QY 241 QWTSKYGSGWGVLWDGYSGVHSADLVPELWAPGGAKQBRLNKEIGDVRARIYRSHLNCTY 300 Db 241 QWTSKYGSGWGVLWDGYSGVHSADLVPELWAPGGAKQBRLNKEIGDVRARIYRSHLNCTY 300 QY 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES 360 Db 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES 360 QY 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTTGGPAGFWES 360 QY 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGBDVYGDAVYFGVVGKSAIGFTSYRGFYRAY 420
Qy 121 KDLYGESLANKKCLGLKEVARVESPHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 Db 121 KDLYGESLANKKCLGLKEVARVESPHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 QY 181 ELVGPPGKVYIKANWKAPARNFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPBGAGL 240 Db 181 ELVGPPGKVVIKANWKAPARNFVGWTHASSLRSGESIFSSLAGNAALPPBGAGL 240 QY 241 QWTSKYGSGMGYLWDGYSGVHSADLVPELMAFGGAKQERIANKEIGDVRABIYRSHLNCTV 300 Db 241 QWTSKYGSGMGYLWDGYSGVHSADLVPELMAFGGAKQERIANKEIGDVRABIYRSHLNCTV 300 CQY 301 PPNNSMLTCSGVPKVWNPIDANTTEVWTYAIVEKOMPEDLIKRRLADSVQRTGGRAGFWES 360 Db 301 PPNNSMLTCSGVPKVWNPIDANTTEVWTYAIVEKOMPEDLIKRRLADSVQRTGGRAGFWES 360 Db 301 PPNNSMLTCSGVPKVWNPIDANTTEVWTYAIVEKOMPEDLIKRRLADSVQRTGGRAGFWES 360	QY 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 Db 361 DDNDNWETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QY 421 QAHVSSSNWAEFEHASSTWHTELFKTTDR 449 Db 421 QAHVSSSNWAEFEHASSTWHTELFKTTDR 449	RESULT 2 US-09-843-250-33 US-09-843-250-33 Federate 33, Application US/09843250 Fublication No. US20030022335A1 GENERAL INFORMATION: APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Resistor, S. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT FILING DATE: 2001-04-26 FRIOR PELICATION NUMBER: US/09/25079 FRIOR PILING DATE: 1999-10-26 FRIOR PILING DATE: 1999-10-26 FRIOR PILING DATE: 1999-10-26 FRIOR PELICATION NUMBER: US 60/105,575 FRIOR APPLICATION NUMBER: US 60/105,575 FRIOR PILING DATE: 1999-10-26	ο ·	Query Match Best Local Similarity 99.8%; Score 2404; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 1.8e-226; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0; QY MNYNNKILVSESGLSOKHLINGDEBLEQHELKTIFARNWLFLTHDSLIPAPGDYVTAKNG 60 DD	61 61 121 121 181

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Sequence 2, Application US/09843250

Sequence 2, Application US/09843250

Publication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Remick, R.

APPLICANT: Gibson, D.

APPLICANT: Remick, S.

APPLICANT: Lee, K.

TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.0064S2

CURRENT PILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: DCT/US99/25079

PRIOR APPLICATION NUMBER: DC 60/105,575

PRIOR PILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 449
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Publication No. US20030022335A1
GRWEAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
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US-09-843-250-2
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ORGANISM: Artificial Sequence
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| Sequence 58, Application US/09843250
| Publication No. US20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Parales, R.
| APPLICANT: Gibson, D.
| APPLICANT: Resmick, S.
| APPLICANT: Resmick, S.
| TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 975.006US2
| CURRENT APPLICATION NUMBER: US/09/843,250
| CURRENT PILING DATE: 1999-10-26
| PRIOR PLILING DATE: 1999-10-26
| PRIOR APPLICATION NUMBER: US 60/105,575
| PRIOR PILING DATE: 1999-10-26
| WUMBER OF SEQ ID NOS: 65
| SOFTHARE: PRAESEQ for Windows Version 4.0
| SEQ ID NO 58
| LENGTH: 449
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                                                                OAHVSSSNWARFEHASSTWHTELTKTTDR 449
                                                                                       QARVSSSNWARFEHASSTWHTBLITKTTDR 449
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ORGANISM: Artificial Sequence
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Sequence 26, Application US/09843250

Sequence 26, Application US/09843250

Sequence 26, Application US/09843250

PUBLICANT: Parales, R.

APPLICANT: Glasson, D.

APPLICANT: Glasson, D.

APPLICANT: Lee, K.

TITLE OF INVENTION: NO. US20030022335Alel naphthalene dioxygenase and methods for the FILE REPERENCE: 875.006402

CURRENT APPLICATION NUMBER: US/09/843,250

CURRENT APPLICATION NUMBER: PCT/US99/25079

FRICE APPLICATION NUMBER: PCT/US99/25079

FRICE APPLICATION NUMBER: US 60/105,575

FRICE APPLICATION NUMBER: US 60/105,575

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 26

LENGTH: 449

TYPE: PRT
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                                                                                                                                                                                           Length 449;
                                                                                                                                                                                                                                      Indels
  ; SEQ ID NO 15
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial Sequence
; PRATURE:
; CHARRIER
; CHARRIER
; US-09-843-250-15
                                                                                                                                                                                         Score 2401; DB 11;
Pred. No. 3.5e-226;
0; Mismatches 1;
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                                                                                                                                                                                         Query Match
Best Local Similarity 99.8%;
Matches 448; Conservative
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Matches 448; Conserva
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Sequence 15, Application US/09843250

Publication Wo. US20030022335A1

Sequence 15, Application US/09843250

Publication No. US20030022335A1

APPLICANT: Parales, R.

APPLICANT: Resmick, S.

APPLICANT: Resmick, S.

TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2

CURRENT APPLICATION NUMBER: 2001-04-26

PRIOR FILING DATE: 1999-10-26

PRIOR PPLICATION NUMBER: PCT/US99/25079

PRIOR APPLICATION NUMBER: PCT/US99/25079

PRIOR APPLICATION NUMBER: DC 10-26

PRIOR APPLICATION NUMBER: DC 10-26

PRIOR APPLICATION NUMBER: DC 10-26

PRIOR PILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PRAEERO for Windows Version 4.0
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US-09-843-250-14
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                CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
FRIOR APPLICATION NUMBER: PCT/US99/25079
FRIOR FILING DATE: 1999-10-26
FRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FILE REFERENCE: 875.006US2
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; Bublication W. US2003022335A1
; GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for t FILE REPRENCE: 875.006U2.
FILE REPRENCE: 875.006U2.
FURRENT APPLICATION NUMBER: US/09/843,250
CURRENT PILING DATE: 2001-04-26
PRIOR PILING DATE: 1999-10-26
PRIOR PILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
SEQ ID NO 35
LENGTH: 449
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                                                                                                                                                     OMISKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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US-09-843-250-35
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ORGANISM: Artificial Sequence
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US-09-843-250-35
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                                               1 MNYNNKILVSBSGLSQKHLIHGDBELPQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG
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                                                                                                                                                                       KOLYGESLNKKCLGLKEVARVESFHGF1YGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
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US-09-843-250-59
Sequence 59, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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	Db 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QY 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 Db 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
	RESULT 12 US-09-843-250-16 September
36 No. US2003022335A1 No. US2003022335A1 Parales, R. Gibson, D. Resnick, S. Lee, K. VENTION: No. US20030022335A1e1	
) LENGTH: 449 ; TYPE: PRT ; ORGANIZAM: Artificial Sequence ; PRATURE: ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:5. US-09-843-250-16
SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 36 ; LENGTH: 449 ; TYPE: PRT	Query Match Best Local S Matches 447
) OXGANISM: Artificial Sequence ; FRATURE: ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:31. US-09-843-250-36	Qy 1 MAYNAKILVSESGLSOKHLIHGDEELFQHELKTIFARNWLFLTHDSLIFARGGYVTAKOG 60
Query Match Best Local Similarity 99.8%; Pred. No. 4.3e-226; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Qy 61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120 bb 61 IDEVIVSRQNDGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
SSGLSQKHLIHGDEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKOG 60 	Qy 121 KDLYGBSLANKKCLGLKEVARVESFHGFIYGCFDQRAPPLMDYLGDAAWYLEPMFKHSGGL 180 121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQRAFPLMDYLGDAAWYLBPMFKHSGGL 180
QY 61 IDBVIVSRQNDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPPE 120 Db 61 IDBVIVSRQNDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120	Qy 181 ELVGPPGKYVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240
QY 121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180 DD 121 KDLYGESLANKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180	Qy 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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CY 241 CMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKGERLAKEIGDVRARIYRSHLNCTV 300 241 CMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300	Qy 361 DDWDWHETASQNGKKYQSRDSDLLSNLGFGEDYYGDAVYPGVVGKSAIGETSYRGFYRAY 420
QY 301 FPNNSMLTCSGVFKVMNPIDANTTEVMTYAIVEKOMPEDLKRRLADSVQRTGGPAGFWES 360	Oy 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 DD 421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
Qy 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420	RESULT 13 US-09-843-250-17

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APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lise, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.0660182
CURRENT PILING DATE: 2001-04-26
PRIOR PILING DATE: 1999-10-26
PRIOR PILING DATE: 1999-10-26
PRIOR PILING DATE: 1999-10-26
RIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FASELSQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 OMTSKYGSGMGVLMDGYSGVHSADLVPBLMAFGGAKQERLNKEIGDVRARIYRSHLNCTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTGGPAGFWES
                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                     Length 449;
                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                        ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:7.
US-09-843-250-18
                                                                                                                                                                                                                                                                                               Query Match 97.2%; Score 2343; DB 11;
Best Local Similarity 96.7%; Pred. No. 1.6e-220;
Matches 434; Conservative 10; Mismatches 5;
               CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1999-10-26
PRIOR PLING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-843-250-19
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                                               APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Lee, K. TITLE OF INVENTION: NO. US20030022335Alel naphthalene dioxygenase and methods for the PILE REPERRNCE: 875.066425 CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT PILING DATE: 1999-10-26 PRIOR APPLICATION NUMBER: US 60/105,575 PRIOR PILING DATE: 1998-10-26 NUMBER OF SEQ ID NOS: 65 NUMBER OF SEQ ID NOS: 65 NUMBER OF SEQ ID NOS: 65 LD NO 17 LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 18, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 IDEVIVSRONDGSIRAFLANCRHRGKTLYSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDLYGESINKKCLGLKEVARVESFHGF!YGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.2%; Score 2391; DB 11; Length 449; 99.3%; Pred. No. 3.3e-225; Live 1; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                              FEATURE:

JOTHER INFORMATION: A polypeptide encoded by SEQ ID NO.6.
US-09-843-250-17
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Sequence 17, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 99.3
Matches 446; Conservative
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US-09-843-250-18
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241 QMTSKYGSGMGVLAPGYSGVHSADLVPELMAFGGAKQERLNKEIGDVPARIYRSHLACTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301 PPNNSVLTCSGVFKVWNPIDANTTEVWTYALVEKDMPEDLKRRLADAVQRTVGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                   61 IDEVIVSRQSDGSIRAFLAVCRHRGKTLVNAEAGNAKGFVCSYHGRGFGSNGELQSVPFE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGBVRARIYRSHLNCTV 300
                                                                                                                                                                                                                                                                                                                                            61 IDEVIVERONDGSIRAFLINVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGBLQSVPFE 120
                                                                                                                                                                                                                                                                                  1 MNYKNKILVSESGLTQKHLIHGBESLFQHELKTIXARNWLFLTHDSLIPSFGDYVTAKMG 60
                                                                                                                                                                                                                                                               1 MIYYNNKILVSESGLSQXHLIHGDEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKWG 60
                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                            Query Match 96.1%; Score 2315; DB 11; Length 449; Best Local Similarity 95.5%; Pred. No. 9.1e-218; Matches 429; Conservative 12; Mismatches 8; Indels 0
                                      FEATURE:

OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:8.

NAME/KEY: SITE

LOCATION: (35)...(35)

OTHER INFORMATION: Xaa = any amino acid.
US-09-843-250-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 QAHVSSSNWARFEDASSTWHTELITKTTDR 449
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TYPE: PRT
ORGANISM: Artificial Sequence
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Search completed: December 9, 2003, 16:09:32 Job time: 23.1429 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

December 9, 2003, 15:44:13 ; Search time 11.8571 Seconds (without alignments) 1602.205 Million cell updates/sec Run on:

US-09-843-250-33 2408 Title: Perfect score:

1 MNYNNKILVSESGLSQKHLI......ABFEHASSTWHTELTKTTDR 449 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 segs, 42310858 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Database :

Bued Patents AA:*
/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		æ			SUMMAKIES		
Result No.	Score	Query	Length DB	DB	a.	Description	
п	407.5	16.9	463	4	US-09-252-991A-31367	Semience 31367. A	
7	407.5	16.9		4	US-09-328-352-6452	6452	
ო	388	16.1	445	4	US-09-328-352-7248	7248	
4	382.5	15.9		4	US-09-252-991A-31385		
ស	360	15.0		4	US-09-328-352-7581	7581.	
ø	344.5	14.3	425	4	US-09-252-991A-25088	25088	
7	291	12.1		ゼ	US-09-252-991A-17164	17164.	
80	278.5	11.6	375	4	US-09-328-352-4700	•	
o,	237.5	9.	529	41	US-09-252-991A-19627		
10	224	9.3	446	4	US-09-004-393B-4	4	
11	223	9.3	439	4	US-09-004-393B-2	ď	
12	185	7.7	32	m	US-08-810-009-19	Sequence 19, Appl	
13	174	7.2		ო	US-08-810-009-20	20	
14	168	7.0		m	US-08-810-009-21	2	
15	143.5	6.0		4	US-09-252-991A-27100		
16	128	5.3		4	US-09-328-352-6765		
17	118.5	4.0		4	US-08-976-063E-4		
18	113,5	4.7		m	US-09-028-934-36		
19	110	4.6	35	m	US-08-810-009-12	12	
70	109	4.5		m	US-08-810-009-14	-	
21	109	4.5	364	4	US-09-328-352-4956	495	
22	108	4.5		ო	US-08-810-009-13	-	
23	108	4.5	35	m	US-08-810-009-15	15	
24	108	4.5		4	US-09-311-626B-4	4	
25	106.5	4.4		m	US-08-809-326A-16	16,	
56	106.5	4.4	432	ぜ	US-09-689-914A-16	16,	
27	106.5	4.4	432	4	US-09-689-913A-16	16,	

Sequence 16, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 15, Appl	Sequence 9, Appli	Sequence 18, Appl	Sequence 11, Appl	ω,	Sequence 10, Appl	44,	45,	Sequence 466, App	Sequence 5961, Ap	Sequence 17, Appl	Sequence 57, Appl	Sequence 6, Appli	Sequence 6, Appli
US-09-689-916A-16	US-08-809-326A-15	US-09-689-914A-15	US-09-689-913A-15	US-09-689-916A-15	US-08-810-009-9	US-08-810-009-18	US-08-810-009-11	US-08-810-009-8	US-08-810-009-10	US-08-810-009-44	US-08-810-009-45	US-09-198-452A-466	US-09-328-352-5961	US-08-810-009-17	US-09-325-932A-57	US-09-036-987A-6	US-09-370-700-6
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432	649	649	649	649	32	35	35	32	35	17	17	1132	363	e C	256	5588	5588
4.4	4.4	4.4	4.4	4.4	4.4	4,3	4.3	4.2	4.5	4.2	4.2	4.2	4.2	4.2	4	4.1	4.1
106.5	106.5	106.5	106.5	106.5	106	104	103	102	102	101	101	101	100.5	100	99.5	98	98
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ALIGNMENTS

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GENERAL INFORMATION:

Patent No. 6521795

GENERAL INFORMATION:

PAPLICATION:

TITLE OF INVENTION:

TITLE OF INVENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               197 APAENFVGDAYHVG---WTHASS------LRSGESIFSSLAGNAALPPEGAGLQ 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16.9%; Score 407.5; DB 4; Length 463; 29.0%; Pred. No. 2e-30; ive 69; Mismatches 149; Indels 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 29.0
Matches 110; Conservative
RESULT 1
US-09-252-991A-31367
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Patent No. 6551795
Sequence 31385, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: DAGGINGNOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/074,788
PRIOR PLILING DATE: 1999-02-18
PRIOR PLILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31385
LENGTH: 466
                                                                                                                                  80 VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                      140 RVESFHGFIYGCFDQBAPPLMDYLGDAAWYLEPMFKHSGG--LELVGP-----PGKVVIK 192
                                                                                                                                                                                                                                                                                                                                                                         294 ---SHINCTVFPNNSMLTCS-GVFKVWNPIDANTTEVWTYAIVEKD----MPEDLKRRLA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 VGGSGFNIALEPIN---IACSMAFFRVIQPISVAETEI-HHSVITMDGGPQIANQYRLRLH 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 BHFQ---GPFGTPDDSEAWERV-GHGAN-AGNDLWIMINRGL------PGEVKT 418
                                                                                                                                                                                                                                                                                                                 -----FEN 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 DSVQRTAGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVG- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV--PPEKDLYGESLNKKCLGLKEVAR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 VESFHGFIYGCFDQEA-PPLMDYLGDAAWYLEPMFKH--SGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 PAENFVGDAYHVGWTHASSIRSGESIFSSLAGNAALPPEGAGLQMT---SKYGSGMGVL- 253
                                                     20 IHGDEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
                                                                                                                                                                                                                                                                     193 ANWKAPAENFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLQMTSKYGS
                                                                                                                                                                                                                                                                                                                                                249 GMGVLWDGYSGVHSADLVPELMAFGGAKQER-LNKEIGDVR------ARIYR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 DEBLEQHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDEVIVSRONDGSIRAFLNVCR
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                                                                                                                                                                                                                                                                                                        220 -NWKIQLEN-TIDAYHFPLVHKSFLSSVDEKTEELFN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.9%; Score 382.5; DB 4; 27.1%; Pred. No. 4.9e-28; tive 77; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 EDGLKSDVSAETGMRAAYQQWK 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            405 ----KSAI-GBISYRGFYRAYQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120; Conservative
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Best Local Similarity
Matches 120; Conserva
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                                                                                                                                Sequence 6452, Application US/09328352

PARENT NO. 6562958

GENERAL INFORMATION:
APPLICAMT: GALY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERABEUTICS
FILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERABEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6452
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Patent No. 6562958
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BUCKEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BUCKEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: BUCKEIC ACID AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKK-CLGLKEVAR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENFVGDAYHVG---WITHASSLRSGESIFSSLAGNAALPPEGA-GLOMISKYG--SGMGVL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 WDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR--IYRSHLNCTVFPNNSMLTCSG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 DEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLAVÇR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
16.9%; Score 407.5; DB 4; Length 496;
Best Local Similarity 31.3%; Pred. No. 2.2e-30;
Matches 105; Conservative 59; Mismatches 146; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
16.1%; Score 388; DB 4; Length 445;
Best Local Similarity 28.1%; Pred. No. 1.4e-28;
Matches 124; Conservative 66; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 -VFKVWNPIDANTTRVWTYAIVEK-DMPEDLKRRL 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 SQIRVLRPLSVNRTEVTIXCIAPKGEAPEARARRI 395
                        || : : | || 374 TPDDLEEFRSCQQG---YQ 389
                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-6452
359 ESDDNDNMETASQNGKKYQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT Acinetobacter baumannii US-09-328-352-7248
                                                                                                                    -09-328-352-6452
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US-09-328-352-7248
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APPLICANT: MATC J. Rubenfield et al.
APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT PELLONG DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85 GAKVCAERQCNGQRFTCPYHGWTYDSHGSLIGLP-DKAAYQHA--GQCHPELSLITRVKHA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVES- 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 FVGDAYHVGWTHASSIRSGESIFSSIAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 SGPPSTGRPIAYWSPLFPEALKPSIAAKFERLVBRFGQARAEDIAHTWKSLFIFPNLVIN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S-----ADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPN---N 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             307 DILCLN--IRSFFPTAADEVSVTVWGAGFADETREERAARINGLISFIGPGGFGTPDDVE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 GV-DAYHLPFAHKRYLEYLNTL--------GTDPESHKRHGRG-EALGNGHALII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 SMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTAGPAGFWESDDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 144 -PHGFIYGCFDQBAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 ELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 ILESCO---RAYAH-----AALGYSDFSRG----MGPATRRHVDEEQNRGFWREW 407
                                                                                                                                                                                                                                                                                                                                                                                                                                 53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.3%; Score 344.5; DB 4;
Best Local Similarity 27.4%; Pred. No. 1.8e-24;
Matches 114; Conservative 71; Mismatches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17164, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-25088
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US-09-252-991A-17164
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                                                                                                                                                                                                                                                                                                                                                    Sequence 7581, Application US/09328352
Patent No. 6562958
GENERAL INVORMATION:
PAPLICANT: Gary L.
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-0-6-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7581
LENGTH: 471
-NCTVPPNNSML-TCSGVFKVWNPIDANTTEVWTYAI-VEKDMPEDLKRRLADSVQRTAG 353
                                                                                                                                   375 VSGMGTPDDLVEFREAQRGFGARRERHSDI--SRGHGKMLBGATPNSQALGIAPLLTGTE 432
                                                                                   --- EYGQARAEWMMHRL 315
                                                                                                                                                                               354 PAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAI---GF 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SFHGFIYGCFDQEA-PPLMDYLGDAAWYLEPWFKHS--GGLELVGPPGKVVIKANWKAPA 199
                                                 --WDGYSGVHS------ADLVPELMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENFVGDAXHVGWTH---ASSLRSGESIFSSLAGNAALPPEGAGLOMT--SKYGSGMGVLW 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DGWFSFKNGHSVLFSDMPNPTVRFGYSTVMPYMVEKYGEKYAEWAMHRLRNLALYPSLFF 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L-TCSGVFKVWNPIDANTIEVWTYAIVEKDMPEDLKRRLADSVORTAGPAGFWESDDNDN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DGYSGVHSADLV-----PELMAFGGAKQERINKEIGDVRARIYRSHL-NCTVFPNNSM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            366 METASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAYQAHVS 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------ VEFREQOKGFOARL- 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23 DEBLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 15.0%; Score 360; DB 4; Length 471; al Similarity 25.8%; Pred. No. 7.16-26; Il4; Conservative 69; Mismatches 181; Indels '
                                                                         DGWFSFANGHSVLFSEMPNPAVRPGYASVMPRLVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -- TEARRNRIROFEDFFNVSGLGTPDDL
                                                                                                                                                                                                                                              TSYRGFYRAYQAHVSSSNWAEF 432
                                                                                                                                                                                                                                                                           433 ITHEGLYVNQHAH-----WRRF 449
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US-09-328-352-7581
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Sequence 19627, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION
TITLE NO. 6551795
GENERAL INFORMATION: RUDENCE All
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUDINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR PILING DATE: 1999-02-18
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19627
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    191 IK--ANWKAPAENFVGDAYHVG#THASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS 248
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                                                                            -----PGFADSVQVDKYWH 231
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                                                sequence 4, Application US/09004393B; Patent No. 6310271; GENERAL INFORMATION:
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ORGANISM: Pseudomonas aeruginosa
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Best Local Similarity 24.9%
Matches 86; Conservative
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US-09-004-393B-4
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| Patent No. 5652958
| GENERAL INFORMATION
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/328,352
| CURRENT FILING DATE: 1999-06-04
| NUMBER OF SEQ ID NOS: 8252
| SEQ ID NO 4700
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                                                                                                                                                                                                                                                                                                                                                                                                                             60 DQRLFBIDMQBIFHKEWLIAGMTCEIPAKGNFLTLQIGKNPVLVIRGAEGQVHAFHNVCR 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 SFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIK-----ANWK 196
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Best Local Similarity 26.2%; Pred. No. 3e-18;
Matches 97; Conservative 57; Mismatches 131; Indels 85
                                                                                                                                                                                                                            Query Match 12.1%; Score 291; DB 4; Length 449; Best Local Similarity 26.4%; Pred. No. 2.6e-19; Matches 111; Conservative 53; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   257 YSGVHSADLVPELMA-FG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Acinetobacter baumannii
US-09-328-352-4700
                                                                TYPE: PRT CORGANISM: Pseudomonas aeruginosa US-09-252-991A-17164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-328-352-4700
SEQ ID NO 17164
LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
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US-08-810-009-19
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TELEX: 5
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GENERAL Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Polynucleotides Encoding Choline
FILE REPERENCE: UP-162
CURRENT APPLICATION NUMBER: US/09/004,3938
CURRENT APPLICATION NUMBER: 60/035,147
PRIOR PELING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 2
LENGTH: 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 EDALTPPSTWYTEPAFYSHELERIFYKGWQVAGYSEQVKEKNQYFTGSLGNVSYLVSRDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 DGSIRAPLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELOSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMD----YLGDA----AWYLEPMFKHSGGLE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 KELGLAPL-KVAEWGPFILISLDRSLDANADVGTEWIGKSAEDVKAHAFDPNLKFTHRSE 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 TLVSVBAGNAKGFYCSYHGWGFGSNGELQSVPFEKDLYGESINKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 BSGLSQKHLIHGDEBLPQHELKTIFARNWIFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 FOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCRHRGK 86
APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
TITLE OF INVENTION: Plants Transformed Therewith
CURRENT APPLICATION NUMBER: 0509/004,393B
CURRENT FILING DATE: 1998-01-08
PRIOR APPLICATION NUMBER: 60/035,147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
9.3%; Score 223; DB 4; Length 439;
Best Local Similarity 30.1%; Pred. No. 7.7e-13;
Matches 58; Conservative 38; Mismatches 83; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 9.3%; Score 224; DB 4; Length 446; Best Local Similarity 27.4%; Pred, No. 6.4e-13; Matches 58; Conservative 37; Mismatches 97; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 P-----PMECNWKVFCDNYLDSSYHVPYAH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09004393B Patent No. 6310271
                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-004-393B-2
                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Beta vulgaris
US-09-004-393B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-004-393B-2
                                                                                                                                                                                                                                                                                                                  LENGTH: 446
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147 FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08810009
Fatent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: GeLL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSER: BRLL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CUNTY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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Patent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: GARY, JOHN
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Miltray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 575102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                       201 NFVGDAYHVGWTH 213
                                                                                                                                                              280 NYLDSSYHVPYAH 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS:
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Best Local Similarity
Matches 65; Conserva
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US-09-252-991A-27100
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| Patent No. 6211437
| GENERAL INFORMATION:
| APPLICANT: Briggs, Steven P. APPLICANT: Johan, Gurmukh S. APPLICANT: Gray, John
| TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
| TITLE OF INVENTION: METHODS AND DISEASE RESISTANCE IN PLANTS
| CORRESPONDENCE ADDRESS:
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: BELL, SELTZER, PARK & GIBSON
| STREET: P.O. Drawer 34009
| CITY: Charlotte
| STREET: WO. 6211437th Carolina
| STREET: WO. 6211437th Carolina
| ZIP: 28234
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                                                                                                                                           COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER LIBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/810,009

FILING DATE: 04-MAR-1997

CLASSIPICATION: 80

ATOCRNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray

REGISTRATION NUMBER: 5718-4

TELECOMMUNICATION INFORMATION:

TELERAMONE: 919-881-3175

TELERAMONE: 919-881-3175

TELERAMONE: 355102

INFORMATION POR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acide

TYPE: A mino acide

TYPE: A mino acide

TYPE: MINORMATION CATABLESTICS:

TYPE: A mino acide

TYPE: A mino acide
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MEDIUM TYPE: Rloppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 NVCRHRGKTLVNAEAGNAKGPVCGYHGWGFGSNGK 35
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: D.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein US-08-810-009-20
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 30, Conserva
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: APPLICATION: APPLICATION NUMBER: US/09/252,991A

CURRENT PPRICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 27100

LENGTH: 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GIDEVIVSRONDGSIRAFLAVCRHRGK--TLVSVEAGNAKGFVCSYHGWGFGSNGELQSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 PFEKDLYGESLNKKCLGLKEVAR--VESFHGFIY---GCFDQEAPPLMDYLGDAAWYLEP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 P------GQRVRGFPCIRRPPVQERHGFVWVWPGAEBGADAALIPRL---EWAESP 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NNKILVSESGLSQKHLI--HGDEELFQHELKTIFARN--WLFLTHDSLIPAPGDYVTAKM 59
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                                                                                                                                                                                                                                                                                                                               Length 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%; Score 143.5; DB 4; ilarity 24.3%; Pred. No. 5.2e-05; Conservative 41; Mismatches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 168; DB 3;
80.0%; Pred. No. 2.9e-09;
tive 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       219 SGESIFSSLAGNAALPP-----EGAGL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: December 9, 2003, 15:45:54 Job time : 13 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27100, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27100
TELECOMMUNICATION INFORMATION TELEPHONE: 919-881-3140 TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                       7.0%
Best Local Similarity 80.0%
Matches 28; Conservative
                                                                      TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-21
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: December 9, 2003, 15:44:13; Search time 11.8571 Seconds

(without alignments)

1602.205 Million cell updates/sec
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(without alignments)

1602.205 Million cell updates/sec
Perfect score: 2408
Sequence: 1 MNYNNKILVSESGLSQKHLI.....AEFEHASSTWHTELTKTTDR 449

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 328717 seq9, 42310858 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: Issued_Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5E_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/GA_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		* Ouerv				
No.	Score	Match	Match Length DB	BB	ID	Description
-	409.5	17.0	463	4	US-09-252-991A-31367	Sequence 31367. A
63	407.5	16.9	496	4	US-09-328-352-6452	_
m	388	16.1	445	4	US-09-328-352-7248	
4	384.5	16.0	466	4	US-09-252-991A-31385	
'n	363	15.1	471	4	US-09-328-352-7581	
9	347.5	14.4	425	4	US-09-252-991A-25088	
7	294	12.2	449	4	US-09-252-991A-17164	
œ	283.5	11.8	375	4	US-09-328-352-4700	-
o	237.5	6.6	529	4	US-09-252-991A-19627	
10	224	9.3	446	4	US-09-004-393B-4	4
11	223	۳, ص	439	₩	US-09-004-393B-2	'n
12	185	7.7	35	ო	US-08-810-009-19	
13	174	7.2	35	ന	US-08-810-009-20	20
14	168	7.0	35	m	US-08-810-009-21	Sequence 21, Appl
15	143.5	0.9	629	4	US-09-252-991A-27100	271
16	128	5.3	392	4	US-09-328-352-6765	_
17	118.5	4.9	354	4	US-08-976-063E-4	-
18	113.5	4.7	379	m	US-09-028-934-36	36
19	110	4.6	35	m	US-08-810-009-12	12
20	109	4.5	35	ო	US-08-810-009-14	Sequence 14, Appl
21	108	4.5	35	w	US-08-810-009-13	13,
22	108	4.5	35	ო	US-08-810-009-15	15,
23	108	4.5	622	₹	US-09-311-626B-4	4
24	106	4.4	35	m	US-08-810-009-9	9
25	106	4.4	364	4	US-09-328-352-4956	9
26	104	4.3	35	m	US-08-810-009-18	_
27	103.5	4.3	432	ന	US-08-809-326A-16	16

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App	App	App	Appl	App]	App]	App]	App	Appli	App	4, Appl	App	1, A	Appl	Appl	, Apr	71,	Appl
16,	16,	16,	ij	15	15,		ч	œ	2	44,	45,	2961	7,	57,	466	283	46,
Sequence	Sequence	Seguence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence
US-09-689-914A-16	US-09-689-913A-16	US-09-689-916A-16	US-08-809-326A-15	US-09-689-914A-15	US-09-689-913A-15	US-09-689-916A-15	US-08-810-009-11	US-08-810-009-8	US-08-810-009-10	US-08-810-009-44	US-08-810-009-45	US-09-328-352-5961	US-08-810-009-17	US-09-325-932A-57	US-09-198-452A-466	US-09-252-991A-28371	US-08-810-009-46
4	4	4	ო	4	4	4.	m	m	m	m	m	4,	٣	4	4	4	٣
432	432	432	649	649	649	649	35	32	35	11	17	363	35	256	1132	395	17
4.3	4.3	4.3	4.3	4.3	4.3	4.3	4.3	4	4.2	4.2	4.2	4.2	4.2	4.1	4.1	4.0	3
103.5	103.5	103.5	103.5	103.5	103.5	103.5	103	102	102	101	101	100.5	100	99.5	66	97.5	95
œ	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 31367, Application US/09252991A

| Sequence 31367, Application US/09252991A
| Sequence 31367, Application US/09252991A
| Sequence 31367, Application US/09252991A
| Sequence 31367, Application US/09252991A
| Sequence 31367, Application US/0925291A
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AUGUSIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AUGUSIC ACID AND AMINOR INVENT: US/09/252,991A
| CURRENT FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| SEQ ID NO 31367
| LENGTH: 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV--PFEKDLYGESLNKKCLG---LKE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 MTSKYGSGMGVLWDGYSGVHSADLVPE-LMAFGGAKQERLNXEIGDVRAR-IYRSHLNCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 HRGAMICRHKSGNRSSYTCPFHGWTFNNSGKLLKVKDPAEAG-YPQGFN--CEGSHDLTR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 VARVESPHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 VEPNNSML-TCSGVFKVMNPIDANTTBVMTYAIVEKDMPEDLKRRLADSVQRTLGPAGFW 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 LYPNVYLMDQFSSQIRJARPLSVDRTEITIYCIAPKGESABARARRIRQYEDFFNVSGMA 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
17.0%; Score 409.5; DB 4; Length 4
Best Local Similarity 29.0%; Pred. No. 2.3e-30;
Matches 110; Conservative 69; Mismatches 149; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31367
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RESULT 4
US-09-252-991A-31385
Sequence 31385, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: 1369-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                               80 VCRHRGKTLVSVEAGNAKGFVCSYHGWGPGSNGELQSVPFEXDLYGESLNKKCLGLKBVA 139
                                                                                                                                        107 RCRHRAATVCEHKKGKTNSFVCPYKGWSYALDGSLRGVP-SPESYGDCLDKSELPLVSL- 164
                                                                                                                                                                                                                                                                                                                           220 -NWKIQLEN-TIDAYHFPLVHKSFLSSVDEKTEELFN------FEN 257
                                                                                                                                                                                                                                                                                                                                                                                         249 GMGVLWDGYSGVHSADLVPELMAFGGAKQER-LNKEIGDVR------ARIYR- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 294 ---SHINCTVFPNNSMLTCS-GVFKVWNPIDANTTBVWTYAIVEKD----MPEDLKRRLA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       374 EHFQ---GPFGFGTPDDSEAWERV-QHGAN-AGNDLWIMINRGL-------PGEVKT 418
                                                                                                                                                                                                        140 RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGG--LELVGP-----PGKVVIK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                    258 OPGFVEDLGNGHSVMVMIPELVDLEEDLMERPIQERFEDLAQALRDEGHEELEVRRIVRA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 VGGSGFWINLFPN---IACSMAFFRVLQPISVABTEI-HHSVITWDGGPQIANQYRLRIH 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 DSVQRTLGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVG- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV--PFEKDLYGESLNKKCLGLKEVAR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 VESFHGFIYGCFDQEA-PPLAMDYLGDAAWYLEPMFKH--SGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 PAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMT---SKYGSGMGVL- 253
                       20 IHGDEELPOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLN 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98
                                                                                                                                                                                                                                  99 HRGATLVRVGKGNQSTFTCPFHAMCYKNDGRLVKVKAPGE---YPEGFDKATRGLKK-AR
                                                                                                                                                                                                                                                                                                 193 ANWKAPAENFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLQMTSKYGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 DEBLECHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   419 BDGLKSDVSAETGMRAAYQQWK 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         405 ----KSAI-GETSYRGFYRAYQ 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-31385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 27.1%
Matches 120; Conservative
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LENGTH: 466
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                                                                                                                                          Sequence 6452, Application US/09328352
Patent No. 6562958
GRAREAL INFORMATION:
PAPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT PILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7248, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/328,352

CURRENT PALING DATE: 1999-06-04

CURRENT PILING DATE: 1999-06-04

SEQ ID NO 7248

LENGTH: 445

TYPE: PRI

CREANISM: Acinetobacter baumannii

US-09-328-352-7248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENFVGDAYHVG---WIHASSLRSGESIFSSLAGNAALPPEGA-GLOMISKYG--SGMGVL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 EN-GADGYHVSAVHWNYAATTQHRKE--TQAADNIRAMSAGSWGKQGGGSYGFENGHMLL 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 254 WDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRAR--IYRSHLNCTVFPNNSMLTCSG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 WIQWANPEDRPUPP-----KADRYTEKYGEAMSKUMIERSR-NLCLYPNVYLMDQFG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDL-YGESLNKK-CLGLKEVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
16.9%; Score 407.5; DB 4; Length 496;
Best Local Similarity 31.3%; Pred. No. 4e-30;
Matches 105; Conservative 59; Mismatches 146; Indels 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.1%; Score 388; DB 4; Length 445;
Best Local Similarity 28.1%; Pred. No. 2.4e-28;
Matches 124; Conservative 66; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 SQIRVLRPLSVNRTEVTIYCIAPKGBAPBARARI 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            312 -VPKVWNPIDANTTEVWTYAIVEK-DMPEDLKRRL 344
                            374 TPDDLEBFRSCQQG---YQ 389
                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TYPE: PRT
2 ORGANISM: Acinetobacter baumannii
US-09-328-352-6452
359 ESDDNDNMETASQNGKKYQ 377
                                                                                                           RESULT 2
US-09-328-352-6452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-328-352-7248
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Sequence 25088 Application US/0925291A

Sequence 25088 Application US/0925291A

SEQUENCE 25088 Application US/0925291A

SEQUENCE 25088 Application US/0925291A

SEQUENCE SELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25088

LENGTH: 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 -FHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWKAPAEN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 VYRNFLFIHYAARQPSLETYLGQAKDYIDLICDQSEAELBIIPGGFEHSIKANWKLLAEN 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 FVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDGYSGVH 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-----ADLVPB-LMAFGGAKQBRLNKBIGDVRAR-IYRSHLNCTVFPN---N 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 SGPPSTGRPIAYWSPLFPBALKPSIAAKFBRLVBRFGQARARDIAHTNKSLFIFPNLVIN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 SMLTCSGVFKVWNPIDANTTEVWTYAIVEXDMPEDLKRRLADSVQRTLGPAGFWESDDND 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   307 DILGIN -- IRSFEPTAADEVSVTVWGAGFADETREERAARINGLISFIGPGGFGTPDDVE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 ELHRRELHEIFDDSWLYAAHLSELREPGDFITRDVGGRNLIIQRRADGEPAVYLNACAHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 BLPQHELKTIFARNWIFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
14.4%; Score 347.5; DB 4; Length 425;
Best Local Similarity 27.4%; Pred. No. 1.5e-24;
Matches 114; Conservative 72; Mismatches 177; Indels 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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                                                                     US-09-252-991A-25088
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APPLICANT: GATY. L. Breton et al.
APPLICANT: GATY. L. Breton et al.
TITLE OF INVENTION: BAUGANII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUGANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: GTC99-03PA
CURRENT REPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7591
                                                                                                                 315
215 QNENGL-DGYHVSTVHYNYV-----ATVQHRQQVBAERGGVAATLDYSKLGAGDAATD 266
                                                                  --WDGYSGVHS-----ADLVPELMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                                                          297 -NCTVPPNNSML-TCSGVFKVMNPIDANTTEVWTYAI-VEXDMPEDLKRRLADSVQRTLG 353
                                                                                                                                                                                 316 RNIALYPSLFVIDQISSQLRIVRPLAMNRTEIVSQCIGVKGESDADRENRIR-QPEDFFN 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 HRGKTLVSVEAGNAKGFVCSYHGMGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 HRGATLTRVAKGNQSTFTCPFHAMCYKSDGRLVKVKAPSE-YCEDFDKSSRGLKQ-GRIA 152
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                                                                                                                                                                                                                                                354 PAGEWESDDWDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAI---GE
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                                                                                                                                                                                                                                                                                                                                                                        433 ITHEGLYNOHAH-----WRRF 449
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                                                                                                                                                                                                                                                                                                                                       411 TSYRGFYRAYQAHVSSSNWAEF 432
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Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 25.8 Matches 114; Conservative
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US-09-328-352-7581
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APPLICATE MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERIGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Sequence 19627, Application US/09252991A

Sequence 19627, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
ALL STATEMENT MALC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNOS: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
SPRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                         232 TTHQNWTLQYG------FARSSEKSFKLDPSVTDPEFHGFWT-WPCTWFNVPPGSN 280
                                                                                                                                                                                                                                         191 IK--ANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS 248
                                                          ----PGFADSVQVDKYWH 231
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                                                                                                          GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVF---PNNS
                                                                                                                                                                                                            306 MITCSGVFKVWNPIDANTTEVWTYAIV-------EKDM------PEDLKRRLADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    173 BRERLFGRLWIFVGFSSMVRERNQFFTRKIAGVPVVVQRTESG-IRAFLMQCPHR-LSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVEAGNAKGFVCSYHGWGFGSNGELQSVPFEXDLYGESLNKKC-LGLKEVARVESFHGFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 ELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHRGKTLV
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9.9%; Score 237.5; DB 4;
Best Local Similarity 24.9%; Pred. No. 5.8e-14;
Matches 86; Conservative 54; Mismatches 139;
                                  194 TETPANWKVIVDNYM-ECYHCGPAH-----
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US-09-004-393B-4
Sequence 4, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
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US-09-252-991A-19627
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334 VORGLKSRGY 343
                                                                                                                                                                                                                                                                                                           348 VORTLGPAGF 357
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US-09-252-991A-19627
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Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps 17;
                                                                                                                                                                                                                                                                                   60 DQRLFBIDMQBIFHKEWLIACMTCBIPAKGNFLILQIGKNPVLVIRGAEGQVHAFHNVCR 119
                                                                                                                                                                                                                                                                                                                                                      83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELOSVPFEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                     143 SFHGFIYGCFDQBAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIK-----ANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       197 APAENFVGDAYHVGWTHASSIRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      331 ----LHL------PHSWNHCMGDHLIVETVW-PISAQETLVTTKWIVHKDAVEGVDYDVB 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 ------DLKRRLADSVQRTLGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     380 RIRBUWDATNDQDRRLABENQRGINSDAYQPGPYSKTYEFGVINFLDHYS--ERMINNLG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFV-CSYHGWGFGSNGELQSV-----PFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GAKO---ERLNKEIGDVRA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 RIYRSHINCTVFPNNSMLTCSG----VFKVWNPIDANTTEVWTYAIVEKDMPE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 VFYTSSQVFEHEKEVIFAKSWICVAHGSELAQPNDYITRKVIGENIVIIRGKDSVLRAFY
                                                                                                                                                                                                                                                      23 DEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLAVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 LIHGDEELFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDEVIVSRQNDGSIRAFL
                                                                                                                                                                                                            Gape
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                                                                                                                                                 12.2%; Score 294; DB 4; Length 449; 26.4%; Pred. No. 2e-19; tive 54; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 YSGVHSADLVPELMA-FG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i ORGANISM: Acinetobacter baumannii
US-09-328-352-4700
                          ; IENGTH: 449
; TYPE: PRT
; ORGANISM: PREDUCMONDAS ABENGINOSA
US-09-252-991A-17164
                                                                                                                                                                                                    Matches 111; Conservative
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 98; Conserv
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US-09-328-352-4700
SEQ ID NO 17164
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147 PIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
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APPLICANT: Daigs, Steven P.
APPLICANT: Dohal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES:
ADDRESSES: BELL, SELTZER, PARK & GIBSON
STRET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Patent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Gray, John
TITLE OF INVENTION: GELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: GELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
AUPLICATION DATE: US/08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 NVCRHRGKTLVSVBAGNAKGPVCSYHGWGFGSNGK 35
                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08810009 Patent No. 6211437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                             280 NYLDSSYHVPYAH 292
                                                                                                                              201 NFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SRQ ID NO:
SEQUENCE CHARACTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 94.3
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , MOLECULE TYPE: protein US-08-810-009-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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; Sequence 2, Application US/09004393B
; Patent No. 6310271
; GENERAL INFORMATION:
    APPLICANT: Hanson D., Andrew
    APPLICANT: Rathinasabapathi, Bala
    APPLICANT: Burnet, Michael
    TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
    TITLE OF INVENTION: Plants Transformed Therewith
    FILE REFERENCE: UF-162
    CURRENT APPLICATION NUMBER: US/09/004,393B
    CURRENT FILING DATE: 1997-01-08
    PRIOR PALLICATION NUMBER: 60/035,147
    PRIOR FILING DATE: 1997-01-08
    SEQ ID NO 2
    LENGTHARE: A39
    MUMBER: A39
    MUMBER: A39
    MUMBER: A39
APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Rathinasabapathi, Bala
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Polynucleotides Encoding Choline Monooxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
FILE REFERENCE: UP-162
CURRENT FILING DATE: 1998-01-08
FRIOR PELING DATE: 1998-01-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 DGSIRAFLNVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 KCLGLKEVARVESFHGFIYGCPDQEAPPLMD----YLGDA----AWYLEPMFKHSGGLB 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87 TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPPEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ESGLSQKHLIHGDEELPQHELKTIPARNWLFLTHDSLIPAPGDYVTAKMGIDBVIVSRQN 70
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Best Local Similarity 30.1%; Pred. No. 1e-12;
Matches 58; Conservative 38; Mismatches 83; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.3%; Score 224; DB 4; Length 446; Best Local Similarity 27.4%; Pred. No. 8.5e-13; Matches 58; Conservative 37; Mismatches 97; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 F-----PMRCNWKVPCDNYLDSSYHVPYAH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 LVGPPGKVVIKANWKAPABNFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Spinacia oleracea
US-09-004-393B-2
                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
US-09-004-393B-2
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459 GDEVITSRHMQNVMAPPFWRMALRGNGL 486.
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Job time : 12 secs
                                               TELECOMMUNICATION INFORMATION;
TELERAX: 919-881-3140
TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27100
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-21
                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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Patent No. 6711437

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.

APPLICANT: Johal, Gurmukh S.

APPLICANT: Johal, Gray, John

TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS

NUMBER OF SEQUENCES: 65

NUMBER OF SEQUENCES: 65

CORRESPONDENCE ADDRESS:

ADDRESSER: BELL, SELTZER, PARK & GIBSON

STREET: P.O. Drawer 34009

CITY: Charlotte

STATE: No. 6211437th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: LEM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFCATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W MUXEN;
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELERAX: 575102
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LEMGTH: 35 amino acids
TYPE: ATRAUBEDNES:
TYPE: ATRAUBEDNES:
TYPE: ATRAUBEDNES:
TYPE: ATRAUBEDNES:
TYPE: ATRAUBEDNES:
TYPE: ATRAUBENES:
TYPE: ATRAUBEDNES:
TYPE: ATRAUPEDNES:
TYPE: ATRAUPENES:
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
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                                CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON STREET: P.O. Drawer 34009
CITY: Charlotte
STAIE: NO. 6211437th Carolina
COUNTRY: USA
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-20
NUMBER OF SEQUENCES:
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                                                                                                                                  CITY: Cha
STATE: NC
COUNTRY:
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US-08-810-009-21
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## Sequence 27100, Application US/09252991A
## SPELICATION WILLIAM OF THE REPRENCE: 107196.136
## TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
## CURRENT APPLICATION NUMBER: US/09/252,991A
## CURRENT FILING DATE: 1999-02-18
## PRIOR FILING DATE: 1998-02-18
## PRIOR FILING DATE: 1998-07-27
## PRIOR FILING DAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60 GIDEVIVSRONDGSIRAFLANVCRHRGK--TLVSVEAGNAKGFVCSYHGWGFGSNGELOSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 P------GQRVRGFPCIRRFPVQERHGFVWVWPGAEEQADAALIPRL---EWAESP 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 NNKILVSESGLSOKHLI--HGDEELFQHELKTIFARN--WLFLTHDSLIPAPGDYVTAKM 59
                                                                                                                                                                                                      Gaps
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ilarity 24.3%; Pred. No. 6.2e-05;
Conservative 41; Mismatches 103; Indels 59.
Query Match
7.0%; Score 168, DB 3; Length 35;
Best Local Similarity 80.0%; Pred. No. 3.6e-09;
Matches 28; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                    79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                   1 NVCRHRGKTIVDAEAGNAKGPVCGYHGWGYGSNGK 35
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December 9, 2003, 15:44:14; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec
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2408
1 MNYNNKILVSESGLSQKHLI......ABFEHASSTWHTELTKTIDR 449
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.cgn2_6/ptodata/1/pubpaa/USO6_NEW_PUB.pep:*
.cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
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.cgn2_6/ptodata/1/pubpaa/NEO7_NEW_PUB.pep:*
.cgn2_6/ptodata/1/pubpaa/NEO8_NEW_PUB.pep:*
.cgn2_6/ptodata/1/pubpaa/NEO8_PUBCOMB.pep:*
.cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		5. Appl	6. Appl	Appli	4. Appl	5. Appl	6. Appl	3. Appl	4, Appl	9, Appl	8, Appl	6. Appl	2. Appl	7. Appl	8. Appl	5
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SUMMARIES		JS-09-843-250-35	JS-09-843-250-36	JS-09-843-250-2	JS-09-843-250-14	JS-09-843-250-15	9-843-250-26	US-09-843-250-33	9-843-250-34	9-843-250-59	9-843-250-58	9-843-250-16	US-09-843-250-32	JS-09-843-250-17	JS-09-843-250-18	01 020 670 00 01
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2223 2220 2220 2220 2220 2220 2220 2220	43-25	43-25	43-25	43-25	43-25	5-242	38-62	5-242	5-242	56-76	6-490	6-491	6-490	6-491	6-490	6-491	6-063	6-490	6-491	6-490	6-491	6-490	6-490	6-491	6-491	24-88	47-54	24-09	6-490	6-491
2223 2220 2220 2220 2220 2220 2220 2220	8-60-	8-60-	8-60-	8-60-	8-60-	19-60	-09-7	18-60	18-60	-10-1	77-60	77-60	77-60	77-60	77-60	77-60	18-97	77-60	77-60	77-60	77-60	77-60	77-60	77-60	77-60	-10-1	-10-0	6-60-	77-60	77-60
2223 95.2 449 2220 92.2 449 2190 92.2 444 73.7 15.7 490 336.5 11.8 451 174 7.2 385 118.5 7.7 35 118.5 7.7 35 118.5 7.7 35 118.5 7.7 35 118.5 4.9 354 1109 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 108 4.5 35 107.5 4.5 35	Š	ġ	Ś	ūS	O.S.	US-(ns-(ns-(ns-(NS-(ns-(ns-(US-(ns-(US-1	us-(ns-(ns-(ns-(Sn.	US-(ns-(ng-(_	US-(ns-(
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	16	11	18	13	20	21	22	23	24	25	56	2,	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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APPLICANT: Parales, R.
APPLICANT: Rebson, D.
APPLICANT: Responder, S.
APLICANT: Lee, K.
TITLE OF INVENTION: NO. US20030022335Alel naphthalene dioxygenase and methods for the FILE REPERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 1999-10-26
PRIOR PELING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR APPLICATION NUMBER: US 60/105,575
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 449;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:30.
US-09-843-250-35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 2408; DB 11;
Best Local Similarity 100.0%; Pred. No. 5.2e-226;
Matches 449; Conservative 0; Mismatches 0;
Sequence 35, Application US/09843250 Publication No. US20030022335A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Resultch, S. APPLICANT: Resultch, S. APPLICANT: Resultch, S. APPLICANT: Resultch, S. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the: TITLE OF INVENTION: NO. US20030022335Alel naphthalene dioxygenase and methods for the: CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT FILING DATE: 1999-10-26 PRIOR FILING DATE: 1999-10-26 PRIOR FILING DATE: 1999-10-26 NUMBER: OS 60/105,575 NUMBER OF SEQ ID NOS: 65 SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                                        360
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QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 DDNDNWETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVCKSAIGETSYRGFYRAY 420
                       241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVPARIYRSHLNCTV
                                                                               PPNNSMLTCSGVPKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVORTLGPAGFWES
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Pred. No. 1e-225;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:1
US-09-843-250-2
                                                                                                                                                                                                                                                                                             421 QAHVSSNWABFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                   421 QAHVSSSNWABFEHASSTWHTELTKTTDR 449
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; Publication No. US20030022335A1
; GENERAL INFORMATION:
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Best Local Similarity 99.8%;
Matches 448; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
US-09-843-250-2
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241
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| Sequence 36, Application WS20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Gibson, D. |
| APPLICANT: Gibson, D. |
| APPLICANT: Resnick, S. |
| APPLICANT: Resnick, S. |
| APPLICANT: Lee, K. |
| TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 |
| TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 |
| FILE REFERENCE: 875.006US2 |
| FILE REFERENCE: 875.006US2 |
| FRICK APPLICATION NUMBER: DCT/US99/25079 |
| PRIOR FILING DATE: 1999-10-26 |
| PRIOR APPLICATION NUMBER: DCT/US99/25079 |
| PRIOR PILING DATE: 1998-10-26 |
| PRIOR FILING DATE: 1998-10-26 |
| PRIOR PILING DATE: 1998-10-26 |
| PRIOR PILING DATE: 1998-10-26 |
| PRIOR PILING DATE: 1998-10-26 |
| FRIOR FILING DATE: 1998-10-26 |
| PRIOR PILING DATE: 1998-10-26 |
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                                                                                               BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGBSIPSSLAGNAALPPBGAGL 240
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Pred. No. 8.1e-226;
1; Mismatches 0;
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Best Local Similarity 99.8%;
Matches 448; Conservative
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US-09-843-250-36
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Sequence 15, Application US/09843250

publication No. US2003022335A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Bene, K.
ITIME OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
CURRENT PELING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: US/09/843,250
CURRENT PILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
PRIOR FILING DATE: 1998-10-26
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:4.
US-09-843-250-15
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ORGANISM: Artificial Sequence
FEATURE:
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US-09-843-250-26
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1G-09-843-250-14

1G-09-843-250-14

1 Sequence 14, Application US/09843250

1 Publication No. US20030022335A1

2 GENERAL INFORMATION:

APPLICANT: Gibson, D.

APPLICANT: Gibson, D.

APPLICANT: Resnick, S.

TITLE OF INVENTION:

TITLE OF INVENTION: NO. US20030022335A1el naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2

CURRENT FILING DATE: 1999-10-26

PRIOR PPLICATION NUMBER: US 60/105,575

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR PELING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR FILING APPLICATION NUMBER: US 60/105,575

PRIOR PRIOR FILING APPLICATION NUMBER: US 60/105,575

TYPE: PRIOR PRIOR FILING APPLICATION NUMBER: US 60/105,575

TYPE: PRIOR PRIOR FILING APPLICATION NUMBER: US 60/105,575

TYPE: PRIOR PRIOR PRIORES PRIORES PRATIER: APPLICATION 
DENDINFETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRY 420
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99.8%; Pred. No. 1e-225;
tive 1; Mismatches 0; Indels 0
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                                                                              OAHVSSSNWAEPEHASSTWHTELTKTTDR 449
                                                                                                      QAHVSSSNWABFEHASSTWHTELTKTTDR 449
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Best Local Similarity 99.8
Matches 448; Conservative
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Sequence 34, Application US/09843250

Sequence 34, Application US/09843250

Sequence 34, Application US/09843250

Sequence 34, Application US-03002233541

GENERAL INFORMATION:

APPLICANT: Parales, R.

APPLICANT: Resnick, S.

APPLICANT: Lespick, S.

TITLE OF INTERFERENCE: 875.006US2

CURRENT APPLICANTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE OF PRIOR TRING DATE: 2001-04-26

FRICE APPLICATION NUMBER: US-04-26

FRICE APPLICATION NUMBER: US-07/US99/25079

FRICE PRICE APPLICATION NUMBER: US-07/US99/25079

FRICE PRICE OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 449

TYPE: PRT

ORGANIZAM: Artificial Sequence
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Best Local Similarity 99.8%; Pred. No. 1.6e-225;
Matches 448; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                    Length 449;
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; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:29
US-09-843-250-34
                                                  FRATURE:
; CTHER INFORMATION: A polypeptide encoded by SEQ ID NO:28.
US-09-843-250-33
                                                                                                                                 Query Match
99.8%; Score 2403; DB 11;
Best Local Similarity 99.8%; Pred. No. 1.6e-225;
Matches 448; Conservative 0; Mismatches 1;
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Fublication No. US20030022335A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the TITLE OF INVENTION NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: DCT/US99/25079
FRIOR APPLICATION NUMBER: US 60/105,575
FRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3-845EQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT PILING DATE: 2001-04-26
FRIOR APPLICATION NUMBER: ET/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Fateseg for Windows Version 4.0
SCATANARE: 4449
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US-09-843-250-26
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US-09-843-250-33
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Sequence 58, Application US/09843250

Sequence 58, Application US/09843250

Bublication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Parales, R.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

TITLE OF INVERTION: No. US20030022335A1el naphthalene dioxygenase and methods for the FILE OF FILE OF FILENCE OF SECTION NUMBER: US/09/843,250

CURRENT FILING DATE: 2001-04-26

PRIOR FILING DATE: 1999-10-26

PRIOR PILING DATE: 1999-10-26

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTMARE: FastSEQ for Windows Version 4.0

SEQ ID NO 58

LENGTH: 449
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PPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES
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                                                                                   ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL
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Pred. No. 2e-225;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:56 US-09-843-250-58
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ORGANISM: Artificial Sequence
FRATURE:
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Best Local Similarity 99.8%;
Matches 448; Conservative
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| Publication Wo. US20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Parales, R. |
| APPLICANT: Resnick, S. |
| APPLICANT: Besnick, S. |
| FRICK PILING DATE: 1999-10-26 |
| PRIOR PILING DATE: 1999-10-
                                                                                                                                                                                                                                                                                                                                                IDEVIVSRONDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
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          MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWIFLTHDSLIPAPGDYVTAKMG
                                BLVGPPCKVVIKANWKAPAENPVGDAYHVGWTHASSLRSGESIPSSLAGNAALPPEGAGL
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99.8%; Score 2403; DB 11; Length 449;
Best Local Similarity 99.8%; Pred. No. 1.6e-225;
Matches 448; Conservative 0; Mismatches 1; Indels 0
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ORGANISM: Artificial Sequence
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Sequence 19, Application US/09843250

Sequence 19, Application US/09843250

Publication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Resnick, R.

APPLICANT: Gibson, D.

APPLICANT: Gibson, D.

APPLICANT: Resnick, S.

APPLICANT: Lee, K.

TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPRENCE: 915.0001-04-26

CURRENT APPLICATION NUMBER: US/09/843,250

CURRENT FILING DATE: 1999-10-26

PRIOR FILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR PLING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 97.5%; Score 2347; DB 11; Length 449; Best Local Similarity 96.7%; Pred. No. 4.6e-220; Matches 434; Conservative 11; Mismatches 4; Indels 0
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US-09-843-250-18
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CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079 [C.
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PastSEQ for Windows Version 4.0
SSOFTWARE: 449
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                    APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Reenick, S.
APPLICANT: Les, K.
TITLE OF INVESTION NO. US20030022335Alel naphthalene dioxygenase and methods for the TITLE OF INVESTION NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: US 60/104-26
FRIOR APPLICATION NUMBER: US 60/105,575
FRIOR APPLICATION NUMBER: US 60/105,575
FRIOR PRIJECTION NUMBER: US 60/105,575
FRIOR PRIJECTION NUMBER: US 60/105,575
FRIOR APPLICATION NUMBER: US 60/105,575
FRIOR PRIJECTION DATE: 1999-10-26
FRIOR FILING DATE: 1999-10-26
FRIOR FILING DATE: 1999-10-26
FRIOR FILING APPLICATION NUMBER: US 60/105,575
FRIOR FILING APPLICATION 
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Publication No. US20030022335Al
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:6.
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            Sequence 17, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
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US-09-843-250-18
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181 ELVGPPGKVVIKANWKAPAENFVCDAYHVGWTHASSLRSGESIFSSLAGNAALPPGGAGL 240
                                                                                                                                                                               121 KOLYGESINKKCLGIKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSCCL 180
                                                                                                                                                                                                                                      301 PPNNSMIJCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTLGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                361 DDNDNAETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                                              Query Match 96.3%; Score 2319; DB 11; Length 449; Best Local Similarity 95.5%; Pred. No. 2.5e-217; Matches 429; Conservative 13; Mismatches 7; Indels 0
TYPE: PRT
COCANISM: Artificial Sequence
FEATURE:
CTHEN INFORMATION: A polypeptide encoded by SEQ ID NO:8.
NAME/KEY: SITE
COCATION: (35)...(35)
CTHEN INFORMATION: Xaa = any amino acid.
US-09-843-250-19
                                                                                                                                                                                                                                                                                                                                                                                                                                       421 OAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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Search completed: December 9, 2003, 16:09:35 Job time: 23.1429 secs

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9, 2003, 15:44:13; Search time 11.8571 Seconds (without alignments) 1602.205 Million cell updates/sec
GenCore version 5,1,6
(c) 1993 - 2003 Compugen Ltd.
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US-09-843-250-36 2408 1 MNYNNKILVSESGLSQXHLI......ARPBHASSTWHTELTKTTDR 449 Title: Perfect score:

Scoring table; Sequence:

328717 seqs, 42310858 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents Ah:*

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| /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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| /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
| /cgn2_6/ptodata/1/iaa/backfiles1.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMADIES

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Description		Segmence	Sequence	Segmence	Sequence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Sequence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Sequence	Segmence	Segmence	
SURMAKIES		US-09-252-991A-31367	US-09-328-352-6452	US-09-328-352-7248	US-09-252-991A-31385	US-09-328-352-7581	US-09-252-991A-25088	US-09-252-991A-17164	US-09-328-352-4700	US-09-252-991A-19627	US-09-004-393B-4	US-09-004-393B-2	US-08-810-009-19	US-08-810-009-20	US-08-810-009-21	US-09-252-991A-27100	US-09-328-352-6765	US-08-976-063B-4	US-09-028-934-36	US-08-810-009-12	US-08-810-009-14	US-08-810-009-13	US-08-810-009-15	US-09-311-626B-4	US-08-810-009-9	US-09-328-352-4956	US-08-810-009-18	
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Score		409.5	407.5	388	386	365	349.5	296	281.5	237.5	224	223	185	174	168	143.5	128	118.5	112.5	110	109	108	108	108	106	106	104	
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Sequence 1	Sequence 1	Sequence 8	Sequence 1	Sequence 4	Sequence 4	Sequence 5	Sequence 1	Sequence 5	Sequence 4	Sequence 2	Sequence 4						
US-09-689-914A-16	US-09-689-913A-16	US-09-689-916A-16	US-08-809-326A-15	US-09-689-914A-15	US-09-689-913A-15	US-09-689-916A-15	US-08-810-009-11	US-08-810-009-8	US-08-810-009-10	US-08-810-009-44	US-08-810-009-45	US-09-328-352-5961	US-08-810-009-17	US-09-325-932A-57	US-09-198-452A-466	US-09-252-991A-28371	US-08-810-009-46
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103.5	103.5	103.5	103.5	103.5	103.5	103.5	103	102	102	101	101	100.5	100	99.5	66	97.5	95
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 31367, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Muchanield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31367
LENGTH: 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            266 ---SFEHGHMLLMSRWAN-----PEDRPAF--ERRAELARDFGEARADWMIENSRNLC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 VPPNNSML-TCSGVFKVMNPIDANTTEVWTYAIVEXDMPEDLKRRLADSVQRTIGPAGFW 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
17.0%; Score 409.5; DB 4;
Best Local Similarity 29.0%; Pred. No. 1.9e-30;
Matches 110; Conservative 69; Mismatches 149;
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ORGANISM: Pseudomonas aeruginosa
RESULT 1
US-09-252-991A-31367
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RESULT 4

US-09-252-991A-31385

US-09-252-991A-31385

Sequence 31385, Application US/09252991A

FROMMER CONTROL OF SELVING

THIRD OF INVENTION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUMBER: 1306

CURRENT FILING DATE: 1099-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                     80 VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
                                                                                                                                                                                                                   140 RVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGG--LELVGP-----PGKVVIK 192
                                                                                                                                                                                                                                                                                                             193 ANWKAPAENFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLQMTSKYGS 248
                                                                                                                                                                                                                                                                                                                                                                                                     249 GMGVIMDGYSGVHSADLVPELMAFGGAKQER-LNKEIGDVR-----ARIYR- 293
                                                                                                                                                                                                                                                                                                                                                                                                                                  258 QPGFVEDLGNGHSVMVMIPELVDLEEDLMERPIQERFEDLAQALRDEGHEELEVRRIVRA 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             294 ---SHINCTVPPNNSMLTCS-GVFKVWNPIDANTTEVWTYAIVEKD----MPEDLKRRLA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          318 VGGSGFNLNLFPN---IACSMAFFRVLQPISVAETEI-HHSVITMDGGPQIANQYRLRLH 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           374 EHFQ---GPFGFGTPDDSEAWERV-QHGAN-AGNDLWIMLNRGL-------PGEVKT 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346 DSVQRTIGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVG- 404
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                               IHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLN
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Best Local Similarity 26.3%; Pred. No. 3.38-28;
Matches 117; Conservative 71; Mismatches 157; Indels 100;
                                                                                                                                                                                                                                                                                                                                                       220 -NWKIQLEN-TTDAYHFPLVHKSFLSSVDEKTEELFN-----
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31385
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                                                                                                                                                      Sequence 6452, Application US/09328352
| Patent No. 6562958
| GENERAL INFORMATION:
| APPLICANT: Gary L. Breton et al. |
| TITLE OF INVENTION: BAUDARNII FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: BAUDARNII FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION: BAUDARNII FOR DIAGNOSTICS AND THERAPEUTICS |
| TITLE OF INVENTION NUMBER: US/09/328,352 |
| CURRENT APPLICATION NUMBER: US/09/328,352 |
| CURRENT APPLICATION DATE: 1999-06-04 |
| NUMBER OF SEQ ID NOS: 8252 |
| SEQ ID NO 6452
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Ratent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: GTC99-0378

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7248

LENGTH: 4455

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
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16.1%; Score 388; DB 4; Length 445;
Best Local Similarity 28.1%; Pred. No. 2e-28;
Matches 124; Conservative 66; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.9%; Score 407.5; DB 4; Length 4 31.3%; Pred. No. 3.3e-30; cive 59; Mismatches 146; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 -VFKVWNPIDANTTEVWTYAIVEK-DMPEDLKRRL 344
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                                    374 TPDDLEEFRSCOOG---YO 389
359 ESDDNDNMETASQNGKKYQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6452
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                                                                                                               RESULT 2
US-09-328-352-6452
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US-09-328-352-7248
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Sequence 25088, Application US/09252991A

Retent No. 6551795
GENERAL INFORMATION: US/09252991A

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARROGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: ARROGINGSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25088
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Sequence 17164, Application US/09252991A

Sequence 17164, Application US/09252991A

Sequence 17164, Application US/09252991A

Sequence 17164, Application US/09252991A

TITLE OF INVENTION: NUCLER CAID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLER CAID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: NUCLER: US/09/252,991A

CURRENT APPLICATION NUMBER: US/09/252,991A

PRIOR APPLICATION NUMBER: US/09/4,190

PRIOR PLING DATE: 1998-02-18

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 GKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVES- 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 S-----ADLVPE-LMAFGGAKOERLNKEIGDVRAR-IYRSHLNCTVFPN---N 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 BLPQHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDEVIVSRQNDGSIRAFLNVCRHR
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14.5%; Score 349.5; DB 4;
Best Local Similarity 27.6%; Pred. No. 8.5e-25;
Matches 115; Conservative 71; Mismatches 177;
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Best Local Similarity
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Patent No. 6562963

GENERAL INFORMATION:

PAPLICANT: GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BADVANNI FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT PILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7581

LENGTH: 471
--ADLVPELMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                            ------ÈYĠQAŘÁEWMHRĽ 315
                                                                                                                                                                   -NCTVPPNNSML-TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTIGP 354
                                                                                                                                                                                                                           -----VSQCIGV 354
                                                                                                                                                                                                                                                              355 AGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYR 414
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15.2%; Score 365; DB 4; Length 471;
Best Local Similarity 26.0%; Pred. No. 3.3e-26;
Matches 115; Conservative 69; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                            355 KG--ESD-----ADRENRIRQFEDFFNVSGMGTPDDL-
                                                                                                                                                                                              316 RMLMLYPSLFVIDQISSQLRIVRDLAWMRTEL----
                                                                                                           267 DGWPSFANGHSVLFSEMPNPAVRPGYASVMPRLVA-
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                                                                           --WDGYSGVHS-----
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US-09-328-352-7581
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Sequence 19627, Application US/09252991A :: Patent No. 6551795
GENERAL INFORMATION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-02-18
RECOR FILING DATE: 1998-02-18
RECOR FILING DATE: 1998-02-18
RECOR FILING DATE: 1998-02-18
RECOR FILING DATE: 1998-02-18
SEQ ID NOS: 33142
SEQ ID NOS: 33142
                                                                                                                                                                                                     TTHQNWTLQXG-------FARSSEKSFKLDPSVTDPEFHGFWT-WPCTMFNVPPGSN 280
                                                                                                                                                                                                                                                                                                                                            191 IK--ANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS 248
                                                    194 TETPANWKVIVDNYM-BCYHCGPAH------PGFADSVQVDKYWH 231
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                                                                                                                                                                                                                                                                                                   306 MLTCSGVFKVWNPIDANTTEVWTYAIV-----BKDM------PEDLKRRLADS
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                                                                                                                                                     249 GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVF---PNNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 ELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDBVIVSRQNDGSIRAFLNVCRHRGKTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 YHVGWTHASS-LRSGESIFSSLAGNAALP------PEGAGLQMTSK----YGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                149 YGCFDQRAPPLMDYLGDAAWYLEPMFKHSGGLE--LVGPPGKVVIKANWKAPAENFVGDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344 NHVPFVHPKTPLPVMTAPVRGLARBAAVPSBVLRLLQBGBTPBLRSLSFPTKAPIQPYKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 CSG---VFKVWNPIDANTTE--VWTYAIVEXDMPEDLKRRLADSVQ 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  432 VRGEHFLLQQYDPVAPGETDYHLWMMTARRKDPKTDFSALLSTLIR 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 9.9%; Score 237.5; DB 4; Local Similarity 24.9%; Pred. No. 5.2e-14; nes 86; Conservative 54; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09004393B Patent No. 6310271
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 WFSDLCEGYGDEH----
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US-09-004-393B-4
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Patent No. 6562958
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPRENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPPEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 APAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVLWDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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                                                                                                                                                                                                                                                                                                                                                              DEBLFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDBVIVSRQNDGSIRAFLNVCR
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                                                                                                                                                                                                             12.3%; Score 296; DB 4; Length 449; 26.7%; Pred. No. 1.1e-19; Live 53; Mismatches 159; Indels
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                                                                   TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                             Query Match
Best Local Similarity 26.7%
Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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Best Local Similarity
Matches 97; Conserv
                                                                                                                                             US-09-252-991A-17164
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SEQ ID NO 17164
LENGTH: 449
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224 FVLISLDRSLEEGGDVGTEWLGTSA---EDVKAHAFDPSLQFI-HRSEFPMESNWKIFSD 279
                                                        147 FIYGCFDQEAPPLMD----YIGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
                                                                                                                                                                                                                                                                                                                                                                                                     | Sequence 19, Application US/08810009 |
| Patent No. 6211437 |
| GENERAL INFORMATION: |
| APPLICANT: Briggs, Steven P. |
| APPLICANT: Gray, John |
| TILLE OF INVENTION: WETHODS AND COMPOSITIONS FOR CONTROLLING |
| TITLE OF INVENTION: WETHODS AND DISEASE RESISTANCE IN PLANTS |
| CORRESPONDENCE ADDRESS: | 65 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEB: BELL, SELTZER, PARK & GIBSON |
| STATE: No. 6211437th Carolina |
| COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILLING DATE: 04-MAR-1997
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 57
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR EQU INO: 19: SEQUENCE CHARACTERISTICS:
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NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                       280 NYLDSSYHVPYAH 292
                                                                                                                                                                                         201 NFVGDAYHVGWTH 213
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## APPLICANT: Hanson D., Andrew
## APPLICANT: Rathinasabapathi, Bala
## APPLICANT: Burnet, Michael
## APPLICANT: Burnet, Michael
## TITLE OF INVENTION: Polymclectides Encoding Choline Monocygenase and
## TITLE OF INVENTION: Plants Transformed Therewith
## TITLE OF INVENTION: Plants Transformed Therewith
## FILE REFERENCE: UP-162
## CURRENT APPLICATION NUMBER: US/09/004,3938
## CURRENT APPLICATION NUMBER: 60/035,147
## PRIOR PILING DATE: 1997-01-08
## NUMBER OF SEQ ID NOS: 6
## SEQ ID NO 4
## INSCRIPT: A46
## TENGTH: 446
## TENGTH: A46
## TE
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Patent No. 6310271

GENERAL INFORMATION:

APPLICANT: Hanson D., Andrew

APPLICANT: Rathinasabapathi, Bala

APPLICANT: Rathinasabapathi, Bala

APPLICANT: Burnet, Michael

TITLE OF INVENTION: Polymucleotides Encoding Choline Monocygenase and

TITLE OF INVENTION: Plants Transformed Therewith

FILE REFERENCE: UP-162

CURRENT APPLICATION NUMBER: US/09/004,393B

CURRENT PILING DATE: 1997-01-08

PRIOR PILING DATE: 1997-01-08

NUMBER OF SEQ ID NOS: 6

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 KCLGLKEVARVESFHGPIYGCFDQEAPPLMD----YLGDA-----AWYLEPMFKHSGGLE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 SILACGSGKKSCFVCPYHGWYCGMGSLAKASKAKP--RQNLDPKELGLVPL-KVAVWGP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87 TLVSVEAGNAKGFVÇSYHGWGFGSNGELQSVPPEKDLYGESLNKKCLGLKEVARVESFHG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 ESGLSOKHLIHGDEELFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 9.3%; Score 224; DB 4; Length 446; Best Local Similarity 27.4%; Pred. No. 7.7e-13; Matches 58; Conservative 37; Mismatches 97; Indels ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 LVGPPGKVVIKANWKAPAENFVGDAYHVGWTH 213
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US-09-004-393B-2
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US-09-004-393B-2
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ORGANISM:
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Sequence 20, Application US/08810009
Sequence 20, Application US/08810009
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: GENERAL METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
                                                                      ö
7.7%; Score 185; DB 3; Length 35; llarity 94.3%; Pred. No. 8.2e-11; Conservative 1; Mismatches 1; Indels
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WINDERS OF SEQUENCES: 65
CORRESPONDENCE ADDRESS: 65
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: 0.0. Lewaer 34009
CITY: Charlotte
STREET: No. 6211437th Carolina
COUNTY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: RP.O. DEVELOR
SOFTWARE: BAPECONE: DEVELOR
COMPUTER: READABLE FORM:
MEDIUM TYPE: RP.O. DEVELOR
COMPUTER: READABLE FORM:
CLASSIPICATION NUMBER: 37097
FILLING DATE: BAPECITON:
NAME: SEQUENCE: 310-681-3176
FILLING DATE: SECUENT: SEC
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RESULT 14

US-08-810-009-21

i Sequence 21, Application US/08810009

i Patent No. 6211437

GENERAL INFORMATION:

APPLICANT: Briggs, Steven P.
APPLICANT: Gradl Gurmukh S.
ADRESSER: Bridl, SELTZER, PARK & GIBSON
STREET: D.O. Drawer 34009

CITY: Charlotte SELTZER, PARK & GIBSON
STATE: No. 6211437th Carolina
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INPORMATION:
NAME: Spruill, W. Murray
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Patent No. 6551795
Generate 27100, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR PILING DATE: 1998-02-18
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 CDEPMVFYRGEDGRVAALBDFCPHRGAPLSLGFVEDG----VLVCGYHGLAMGEDGRTRAM 360
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408 DWAYGGGL-----YHIHCDYRLMIDNLM-DLTHETYVHASSIGQKEIDEAAPTTRVE 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 MPKHSGGLELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSL----
                                                                                                                                                                                                                                                                                                                                                     Query Match 7.0%; Score 168; DB 3; Length 35; Best Local Similarity 80.0%; Pred. No. 3.4e-09; Matches 28; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                        79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFA: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Pseudomonas aeruginosa
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                        TYPE: anino acid STRANDEDNESS:
TOPOLOGY: linear
WOLKCULE TYPE: protein US-08-810-009-21
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US-09-252-991A-27100
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December 9, 2003, 15:44:14; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec
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" cgm2_6/ptodata1/pubpaa/US07 PUBCCMB pep: *

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" cgm2_6/ptodata1/pubpaa/US08 PUBCMB pep: *

" cgm2_6/ptodata1/pubpaa/US08_PUBCMB pep: *

" cgm2_6/ptodata1/pubpaa/US09_PUBCOMB pep: *

" cgm2_6/ptodata1/pubpaa/US00_PUBCOMB pep: *

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-843-250-14
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                                                                                     OM protein - protein search, using sw model
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Sequence 20, Appl	Sequence 21, Appl	Sequence 22, Appl	Sequence 23, Appl	Sequence 24. Appl	Sequence 10253, A	Sequence 6140, Ap		n,	Sequence 14477, A	Sequence 19, Appl	19,	Sequence 20, Appl	20,	21,	7		12	12	14	74	13	15,	Sequence 13, Appl	15	4	78	Segmence 15, Appl		
1 US-09-843-250-20	1 US-09-843-250-21	1 US-09-843-250-22	1 US-09-843-250-23	1 US-09-843-250-24	US-09-815-242-10253	0 US-09-738-626-6140	US-09-815-242-11692	US-09-815-242-5097	5 US-10-156-761-14477	US-09-776-490-19	US-09-776-491-19	US-09-776-490-20	US-09-776-491-20	US-09-776-490-21	US-09-776-491-21	US-08-976-063C-4	US-09-776-490-12	US-09-776-491-12	US-09-776-490-14	US-09-776-491-14	US-09-776-490-13	US-09-776-490-15	US-09-776-491-13	US-09-776-491-15	5 US-10-124-880-4	1 US-10-047-542-78) US-09-924-097-15	Þ	
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ALIGNMENTS

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APPLICANT: Barales, R.
APPLICANT: Barales, R.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REPERBORGE: 375.06GUS2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 1909-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PASTESQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 449
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100.0%; Score 2408; DB 11; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.9e-226;
Matches 449; Conservative 0; Mismatches 0; Indels 0;
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US-09-843-250-36
                  Sequence 36, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
US-09-843-250-36
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		and methods for the SECTIONS 165 STORES OF SECTIONS 165 STORES OF SECTIONS 165 STORES OF SECTION 167 STORES OF SECTION 187 SEC	Query Match 100.0%; Score 2407; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 2.4e-226; Matches 448; Conservative 1; Mismatches 0; Indels 0; Gaps Qy MNYNNKILVSSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG Db MNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG Db DNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DK DNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DK DNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DK DNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DK DNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DK DNYNNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DNYNKILVSBSGLSQKHLIHGDBELFQHELKTIFARNMLFLTHDSLIFAPGDYVTAKNG DNYNKILVSBSGLSQKHLIHGTH DNYNKILVSBSGLSQKHLIHGTH DNYNKILVSBSGLSQKHLIHGTH DNYNKILVSBSGLSQKHLIHGTH DNYNKILVSBSGLSQKHLIHGTH DNYNKILVSBSGLSQKHLIHGTH DNYNKILVSBSGLSQKHLIHGTH D	Compact Comp	60 QY 181 120 QY 181 120 QY 241 180 Db 241
KDLYGESLAKKCLGLKEVARVESFHGFIYGCFDQEAPPLADYLGDAAWYLEPMF [361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRG	0. US20030022335A1. 06US2 06US2 2001-04-26 BER: PCT/US99/2507. 98_10-26 98_10-26	OFINATE: FABLESC IOF WINDOWS VERBION 4.0 LENOTH: 449 TYPE: PRT PRATURE: OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:1 0-843-250-2	100.0%; Score 2407; DB 11; Length 449; Similarity 99.8%; Pred. No. 2.4e-226; Indels 0; 89; Conservative 1; Mismatches 0; Indels 0; MYXNKILVSESGLSQKHLIHGDEBLFQHELKTIFARNWLFLTHDSLIFARDDY	MNYMNKILVSESGISQKHLIHGDEELFQHEIKTIFARNNLFLTHDSLIFAPGBYVTALNG IDEVIVSRQNDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGMGFGSNGELGSVPFE

for the:

us-09-843-250-36.rapb

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Squence 35, Application US/09843250

Squence 35, Application US/09843250

Squence 35, Application Wo. US200302235A1

SGUENCAL INFORMATION:

APPLICANT: Paralles, R.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006U32

CURRENT FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: DCT/US99/25079

PRIOR APPLICATION NUMBER: DCT/US99/25079

PRIOR PILING DATE: 1998-10-26

PRIOR PILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

SRIOR FILING DATE: 1998-10-26

SRIOR FILING DATE: 1998-10-26

SRIOR PILING DATE: 1998-10-2
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US-09-843-250-35
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Publication No. US20030022335Al
GENBRAL INFORMATION:
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                        APPLICANT: Parales, R. APPLICANT: Glbson, D. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE OF INVENTION: US004.26 CURRENT FILING DATE: 1901-04-26 CURRENT FILING DATE: 1999-10-26 PRIOR FILING DATE: 1999-10-26 PRIOR FILING DATE: 1998-10-26 SOFTWARE: PastSRQ for Windows Version 4.0 SRQ ID NO 15 LENGTH: 449
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Best Local Similarity 99.8%; Pred. No. 2.4e-226;
Matches 44%; Conservative 1; Mismatches 0; Indels 0;
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OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:4.
                                                                                                        421 QAHVSSSNWABFBHASSTWHTBLTKTTDR 449
                                                                              421 OAHVSSSNWAEPEHASSTWHTELTKTTDR 449
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                                                                                                                                                                                                                                                      Sequence 15, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Sequence 34, Application US/09843250

Sequence 34, Application US/09843250

Publication No. US20030022335A1

GENERAL INPORMATION:

APPLICANT: Parales, R.

APPLICANT: Gibson, D.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the:

TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the:

FILE REFERENCE: 159. NOGEUS.

CURRENT FILING DATE: 2001-04-26

PRIOR APPLICATION NUMBER: US/09/943,250

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 34

LENGTH: 449
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                                                   FEATURE:
; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:28.
US-09-843-250-33
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                                                                                                                                     Query Match 99.8%; Score 2403; DB 11;
Best Local Similarity 99.8%; Pred. No. 5.9e-226;
Matches 448; Conservative 0; Mismatches 1;
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               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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| Publication No. US20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Paralles, R.
| APPLICANT: Gibson, D.
| APPLICANT: Lee, K.
| TITLE OF INVENTION: NO. US20030022335A1e1 naphthaleme dioxygenase and methods for the TITLE OF INVENTION: NO. US20030022335A1e1 naphthaleme dioxygenase and methods for the PILIC OF INVENTION: NO. US20030022335A1e1 naphthaleme dioxygenase and methods for the PILIC OF INVENTION: B75.006US2
| CURRENT APPLICATION NUMBER: US/09/843,250
| CURRENT FILING DATE: 1999-10-26
| PRIOR FILING DATE: 1999-10-26
| PRIOR FILING DATE: 1998-10-26
| PRIOR FILING DATE: 1998-10-26
| NUMBER OF SEQ ID NOS: 65
| SOFTWARE: FRASESQ for Windows Version 4.0
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Pred. No. 4.7e-226;
0; Mismatches 1; Indels 0
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FILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
FRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 26
SEQ ID NO 26
SEQ ID NO 26
SEQ IP NO 26
TYPE: PRI
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Best Local Similarity 99.8%;
Matches 448; Conservative
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LENGTH: 449
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MAYNAKILVSESGLSQKHLIHGDESLFCHELKTIFARNWLFLTHDSLIPAPGDYYTAKMG 60	Qy 121 KDLYGESINKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPWFKHSGGL 180 Db 121 KDLYGESINKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPWFKHSGGL 180 QY 181 ELVGPPGRVYIKANWKAPAENPYGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 Db 181 ELVGPPGRVYIKANWKAPAENFYGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGL 240 CA 241 QWTSKYGSGMGYLWDGYSGVHSADLVPELMAFGGAKQBRLNKEIGDVRARIYRSHLNCTV 300 Db 241 QWTSKYGSGMGYLWDGYSGVHSADLVPELMAFGGAKQBRLNKEIGDVRARIYRSHLNCTV 300 CQY 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYALVEKDWPEDLKRRIADSVQRTIGPAGFWES 360 Db 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYALVEKDWPEDLKRRLADSVQRTYGPAGFWES 360 QY 361 DDNDNMETASQNGKKYGSRDSDLLSNLGFGBDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QY 421 QAHVSSSNWABFBHASSTWHTELTKTTDR 449 Db 421 QAHVSSSNWABFBHASSTWHTELTKTTDR 449
	RESULT 10 US-09-843-250-16 ; Sequence 16, Application US/09843250 ; Publication No. US2003002235A1 ; GENERAL INFORMATION: ; APPLICANT: Parales, R. ; APPLICANT: Glabon, D.
RESULT 9 US-09-843-250-59 is Sequence 59, Application US/09843250 j Fublication No. US2030022335A1 GENERAL INFORMATION: j APPLICANT: Parales, R. j APPLICANT: Resnick, S. j APPLICANT: Lee, K. j TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the TITLE OF INVENTION: No. US20030022335A1el naphthalene dioxygenase and methods for the TITLE OF INVENTION: NO. US20030022335A1el naphthalene dioxygenase and methods for the FILING DATE: 1001-04-26 j CURRENT FILING DATE: 2001-04-26 j PRIOR FILING DATE: 1999-10-26 j PRIOR FILING DATE: 1999-10-26 j PRIOR FILING DATE: US 60/105,575 j PRIOR FILING DATE: US 60/105,575	80
# MONDAY OF SAY ID NOS: 05 # SOFTWARE: FastSRQ for Windows Version 4.0 # SRQ ID NO 59 # LENGTH: 449 # TYPE: PRT	Query Match 99.8%; Score 2402; DB 11; Length 449; Best Local Similarity 99.6%; Pred. No. 7.46-226; Matches 447; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
) ORGANISM: Artificial Sequence) FEATURE:) OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:57. US-09-843-250-59	Qy 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
Query Match Query Match Best Local Similarity 99.8%; Pred. No. 5.9e-226; Matches 448; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	61 IDEVIVSRONDGSIRAFLNYCHRGKTLVGVEAGNAKGEVCSYHGWGFGSNGELOSVPFE
QY 1 MAYANKILVSESGLEOKHLIHGDERLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60	121
Qy 61 IDEVIVSRQNDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELGSVPFB 120 	Cy 181 BLVGPGKVVIKANNKAPABNFVGDAYHVGWTHASSIRSGESIFSSLAGNAALPPBGAGL 240

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USC-09-843-250-32

| Sequence 32, Application US/09843250 |
| Sequence 32, Application WS/09843250 |
| Publication No. US20030022335A1 |
| Publication No. US20030022335A1 |
| APPLICANT: Parales, R. |
| APPLICANT: Gibson, D. |
| APPLICANT: Lee, K. |
| TILE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the PILE REFERENCE: 975.006782 |
| CURRENT FILING DATE: 2001-04-26 |
| PRIOR FILING DATE: 1999-10-26 |
| PRIOR FILING DATE: 1999-10-26 |
| PRIOR FILING DATE: 1998-10-26 |
| SEQ ID NO 32 |
| LENGTH: 449
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361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:27.
US-09-843-250-32
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                                                            421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                           421 QAHVSSSNWARFEHASSTWHTELTKTTDR 449
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ORGANISM: Artificial Sequence
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US-09-843-250-17
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| Sequence 58 Application No. US200302235A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Brailes, R. |
| APPLICANT: Resnick, S. |
| APPLICANT: Resnick, S. |
| APPLICANT: Resnick, S. |
| TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 |
| CURRENT PAPLICATION NUMBER: US/09/843,250 |
| PRIOR PILING DATE: 1999-10-26 |
| WHORE OF SEQ ID NOS: 65 |
| SOFTWARE: FastsEQ for Windows Version 4.0 |
| SEQ ID NO 58 |
| LANGTH: 449 |
| LANGTH: 440 |
| LANGTH: 440
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                                                                                                 360
                                                                                                                           301 FPNNSMLTCSGVFKVWNPIDANTTEVWTYALVEKDMFEDLKRRLADSVQRTVGPAGFWES 360
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                                  OMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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Best Local Similarity 99.8%; Pred. No. 9.3e-226;
Matches 448; Conservative 0; Mismatches 1; Indels 0
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US-09-843-250-58
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US-09-843-250-58
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Publication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Parales R.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for t FILE REFERENCE: 875.060425

CURRENT APPLICATION NUMBER: US/09/843,250

CURRENT FILING DATE: 2001-04-26

PRIOR PELICATION NUMBER: PCT/US99/25079

PRIOR PELICATION NUMBER: US 60/105,575

PRIOR FILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                           Length 449;
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                                                                                                                                                                                          TYPE: PRT
OCGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:7.
US-09-843-250-18
                                                                                                                                                                                                                                                                                                         Query Match 97.5%; Score 2349; DB 11;
Best Local Similarity 96.7%; Pred. No. 1.1e-220;
Matches 434; Conservative 11; Mismatches 4;
 CURENT APPLICATION NUMBER: US/09/843,250
CURENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1999-10-26
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 449
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US-09-843-250-19
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                                             APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 975.006US2
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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Publication No. US20030022335A1
GENERAL INFORMATION:
APPLICANT: Barales, R.
APPLICANT: Gibson, D.
APPLICANT: Lee, K.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
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US-09-843-250-17
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Pred. No. 2.3e-225;
2; Mismatches 1;
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Sequence 17, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.3%;
Matches 446; Conservative
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US-09-843-250-18
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                                                                                                                                                Query Match

96.4%; Score 2321; DB 11; Length 449;
Best Local Similarity 95.5%; Pred. No. 6.1e-218;
Matches 429; Conservative 13; Mismatches 7; Indels 0
TYPE: PRT
COGANISM: Artificial Sequence
COGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: A polypeptide encoded by SEQ ID NO:8.
NAME/KEY: SITE
COTHER INFORMATION: (35)...(35)
OTHER INFORMATION: Xaa = any amino acid.
US-09-843-250-19
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Search completed: December 9, 2003, 16:09:36 Job time : 23.1429 secs

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December 9, 2003, 15:44:14; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO6_NEW PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO7_NEW PUB.pep:*
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| cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
| cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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2410
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Sequence					Seguence	Seguence	Seguence	Seguence	Sequence	Sequence	Segmence	Segmence	Sequence
Summaries Id	US-09-843-250-26	US-09-843-250-58	US-09-843-250-35	US-09-843-250-36	US-09-843-250-2	US-09-843-250-14	US-09-843-250-15	US-09-843-250-33	US-09-843-250-34	US-09-843-250-32	US-09-843-250-16	US-09-843-250-17	US-09-843-250-18	US-09-843-250-19
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Sequence 20, Appl Sequence 21, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl		Sequence 19, Appl Sequence 20, Appl Sequence 20, Appl Sequence 21, Appl Sequence 21, Appl Sequence 4, Appl	,ិកិត្តិកំពី ក ិ	00
11 US-09-843-250-20 11 US-09-843-250-21 11 US-09-843-250-22 11 US-09-843-250-23 11 US-09-843-250-23	9 US-09-815-242-10253 10 US-09-738-626-6140 9 US-09-815-242-11692 9 US-09-815-242-5097 15 US-10-156-761-14477 9 US-09-776-490-19	9 US-09-776-491-19 9 US-09-776-490-20 9 US-09-776-490-21 9 US-09-776-491-21 8 US-08-976-063C-4 10 US-09-924-092-15	555555	9 US-09-776-491-15 15 US-10-124-880-4 14 US-10-047-542-78 9 US-09-776-491-9 9 US-09-776-491-9
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ALIGNMENTS

RESULT 1 US-09-843-250-26 US-09-843-250-26 Sequence 26, Application US/09843250 Publication No. US20030022335Al GENERAL INFORMATION: APPLICANT: Parales, R. APPLICANT: Bareles, R. APPLICANT: Lee, R. APPLICANT: Lee, R. TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT APPLICATION NUMBER: US/09/843,250 CURRENT APPLICATION NUMBER: DCT/US99/25079 PRIOR APPLICATION NUMBER: PCT/US99/25079 PRIOR APPLICATION NUMBER: PCT/US99/25079 PRIOR PILING DATE: 1998-10-26 NUMBER OF SEQ ID NOS: 65 SOUTHARE FASTERQ for Windows Version 4.0 SEQ ID NO 26 LENGTH: 449 LENGTH: 449 TYPE: PRT ORGANISM: Pseudomonas sp.
US-09-843-250-26 Query Match Beet Local Similarity 100.0%; Score 2410; DB 11; Length 449; Matches 449; Conservative 0: Mismatches 0: Indels 0: Gans 0:
MNYNKIIASESGISQKHIJHGDEELFOHELKTIFARNWIFELTHDSLIPAPGDYVTAKOG 60
61 IDBVIVSRQNDGSTRAFLAVCRHRGKTIVSVRAGNAKGFVCSYHGWGFGSNGELQSVPFE
121 KDLYGESLNKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL

	Db 241 QMTSKYGSGWGVLMDCYSGVHSADLVPEL Qy 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTY Db 301 FPNNSMLTCSGVFKVWNPIDANTTEVWTY Qy 361 DDNDNMETASQNGKKYQSRDSDLLSNLGFK DDNDNMETASQNGKKYQSRDSDLLSNLGFK DDNDNMETASQNGKKYQSRDSDLLSNLGFK QAHVSSSNWAEFEHASSTWHTELTKFTDR DDNDNWETASQNGKKYQSRDSDLLSNLGFK	QMTSKYGSGWGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMFEDLKRRLADSVQRTFGPAGFWES 360 FPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMFEDLKRRLADSVQRTYGPAGFWES 360 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
	RESULT 3 US-09-843-250-58 Sequence 58, Application US/09843250 Publication No. US2003002233541 GENERAL INFORMATION: APPLICANT: GIDSON, D. APPLICANT: Renick, S.	13250
RESULT 2 US-09-843-250-59 US-09-843-250-59 Sequence 59, Application US/09843250 Publication No. US20030022335A1 Publication No. US20030022335A1 APPLICANT: Parales, R. APPLICANT: Resnick, S. APPLICANT: Resnick, S. TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods CURRENT PAPLICATION NUMBER: US/09/843,250 CURRENT FILING DATE: 2001-04-26 PRIOR APPLICATION NUMBER: PCT/US99/25079 PRIOR APPLICATION NUMBER: US 601.05.575	ZMMUHZHZWWWW (0022335Alel naphthalene dioxygenase and methods for the 709/843,250 1599/25079 1599/25079 1705,575 16rsion 4.0
PRIOR FILING DATE: 1998-10-26 ; NUMBER OF SEQ ID NOS: 65 ; SEQ ID NO 59 ; LENGTH: 449 ; TYPE: PRT ; OGGNISM: Artificial Sequence ; RATURE: ; PRATURE: ; PRATURE: ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:57.	US-09-843-250-58 Query Match Best Local Similarity 99.8%; Matches 448; Conservative Qy 1 MNYNNKILVSESGLSQKHL. Db 1 MNYNNKILVSESGLSQKHL.	TE 2405; DB 11; TE 2405; DB 11; Mismatches 0; MLSTRIPHELKTIFARNWLE
Ouery Match 99.9%; Score 2407; DB 11; Length 449; Best Local Similarity 99.8%; Pred. No. 1.8e-226; Matches 448; Conservative 1; Mismatches 0; Indels 0; Gaps Matches	OY	IDBVIVSRQNDGSIRAFLNVCRHRGKTLVSVBAGNAKGFVCSYHGWGFGSNGELQSVPFE 120
61 61 121 121 181 181	181 181 241 301 361	
QY 241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQBRLNKEIGBVRARIYRSHLMCTV 300	DD 361 DDNDNWETASQNGKKYQSRI	DDNDNMETASQNGKKYQRDSDLJSNLGFGEDYYGDAYYPGYVGKSAIGETSYRGFYRAY 420

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APPLICANT: Parales, R. APPLICANT: Glbson, D. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH: 449
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Publication No. US20030022335A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TILLE OF INFORMATION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.8%; Score 2404; DB 11; Best Local Similarity 99.8%; Pred. No. 3.6e-226; Matches 448; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: A polypeptide encoded by US-09-843-250-36
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
Publication No. US20030022335A1
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                                                                                                                                                                         Publication No. US20030022335A1

| Publication No. US20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Parales, R. |
| APPLICANT: Gibson, D. |
| APPLICANT: Remick, S. |
| APPLICANT: Lee, K. |
| TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2 |
| CURRENT APPLICATION NUMBER: US,09/843,250 |
| PRIOR APPLICATION NUMBER: PCT/US99/25079 |
| PRIOR PILING DATE: 1999-10-26 |
| PRIOR FILING DATE: 1998-10-26 |
| PUBLICATION NUMBER: WE GOVERNOR OF SEQ ID NOS: 65 |
| PUBLICATION NUMBER: WE SEQ ID NOS: 65 |
| PUBLICATION NUMBER: WE SEG FOR WINGOWS VERSION 4.0 |
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                                                         421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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; Sequence 36, Application US/09843250
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APPLICANT: Farales, R.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Resenick, S.
APPLICANT: Resenick, S.
APPLICANT: Lose, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the:
TILE REFERENCE: 875.0060582
CURRENT FILING DATE: 875.0060582
CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR PLING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH 449
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           ; TYPE: PRT
; ORGANISM: Artificial Sequence
; FRATURE:
; CTHER INFORMATION: A polypeptide encoded by SEQ ID NO:3.
US-09-843-250-14
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                                                                                                                           Score 2403; DB 11;
Pred. No. 4.5e-226;
0; Mismatches 1;
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Best Local Similarity 99.8%; Pred. No. 4.5e-226;
Matches 448; Conservative 0; Mismatches 1;
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                                                                                                                        Query Match
Best Local Similarity 99.8%;
Matches 448; Conservative
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ORGANISM: Artificial Sequence
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APPLICANT: Parallow:
APPLICANT: Balbon, D.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REPERENCE: 915.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001.04-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
RIOR APPLICATION NUMBER: US 60/105,575
RUMBER: OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                ) OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:1
US-09-843-250-2
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 449
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Publication No. US20030022335A1
GENERAL INFORMATION:
                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-843-250-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:29 US-09-843-250-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 34, Application US/09843250
Sequence 34, Application US/09843250
Publication No. US20030022335A1
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT PILING DATE: 2001.04.26
FRIOR APPLICATION NUMBER: PCT/US99/25079
FRIOR APPLICATION NUMBER: PCT/US99/25079
FRIOR APPLICATION NUMBER: US 60/105,575
FRIOR FILING DATE: 1998-10.26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: FastESE for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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TUTREN APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SEQ ID NOS: 65
LENGTHRE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
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                     MYNNKILVSESGLSOKHLIHGDEELFQHELKTIFARNWLFLTHDSLIFAPGDYVTAKMG
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US-09-843-250-33
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ORGANISM: Artificial Seguence
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Best Local Similarity
Matches 448; Conservat
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US-09-843-250-33
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APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Bandok, S.
APPLICANT: Gibson, D.
APPLICANT: Lee, K.
APPLICANT: Lee, K.
TITLE NO INVANTION: NO. US20030022335Alel naphthalene dioxygenage and methods for the FILE REFERENCE: 875.0064923
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
ROPEROR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
LENGTH: 449
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US-09-843-256-16
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                                       421 QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                           421 OAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                                                                                     US-09-843-250-16
; Sequence 16, Application US/09843250
; Publication No. US20030022335A1
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-843-250-17
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301 PPNNSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKKRLADSVQRTTGPAGFWES 360
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US-09-843-250-32
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APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Reson, D.
APPLICANT: Reson, D.
APPLICANT: Reson, C.
APPLICANT: Reson, D.
APPLICANT: Liee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR PEDLICATION NUMBER: US 60/105,575
PRIOR APPLICATION NUMBER: US 60/105,575
NUMBER OF SEQ ID NOS: 65
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                              Length 449;
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; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:7.
US-09-843-250-18
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Best Local Similarity 96.7%; Pred. No. 2.1e-220;
Matches 434; Conservative 10; Mismatches 5;
      CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR PILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 449
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                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Sequence 17, Application US/09843250

Publication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Parales, R.

APPLICANT: Resulcs, R.

APPLICANT: Resulcs, R.

APPLICANT: Resulcs, R.

TITLE OF INVENTION: NO. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPRENCE: 975.006426

FILE REPRENCE: 975.006426

CURRENT FILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: US/09/43,250

CURRENT FILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PastSEQ for Windows Version 4.0
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Publication No. US20030022335A1
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OP INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2
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99.3%; Score 2393; DB 11; Length 449;
Best Local Similarity 99.3%; Pred. No. 4.3e-225;
Matches 446; Conservative 1; Mismatches 2; Indels 0
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US-09-843-250-17
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ORGANISM: Artificial Sequence
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US-09-843-250-18
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241 QMTSKYGSGMGVLMDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVPARIYRSHLNCTV 300°
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                                         FRATURE:
CTHER INFORMATION: A polypeptide encoded by SEQ ID NO:8.
NAME/KEY: SITE
COCATION: (35)...(35)
OTHER INFORMATION: Xaa = any amino acid.
US-09-843-250-19
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               TYPE: PRT
ORGANISM: Artificial Sequence
LENGTH: 449
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Search completed: December 9, 2003, 16:09:31 Job time : 23.1429 secs

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OM protein - protein search, using sw model

December 9, 2003, 15:44:13 ; Search time 11.8571 Seconds (without alignments) 1602.205 Million cell updates/sec Run on:

US-09-843-250-26 2410 1 MNYNNYILVSESGLSQXHLI......AEFEHASSIWHTELTKTTDR 449 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

328717 seqs, 42310858 residues Searched:

328717

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

IsBued Patents AA:*
1: /cgm2_6/ptcdata/1/laa/5A_COMB.pep:*
2: /cgm2_6/ptcdata/1/laa/5B_COMB.pep:*
3: /cgm2_6/ptcdata/1/laa/6A_COMB.pep:*
4: /cgm2_6/ptcdata/1/laa/6B_COMB.pep:*
5: /cgm2_6/ptcdata/1/laa/PcTUS_COMB.pep:*
6: /cgm2_6/ptcdata/1/laa/PcTUS_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Secuence 31367. A				-	-		4700.		4		Seminary 19 Print	2		Segrence 27100 a			Semience 36 ann		4	Semience 12 and		Semience 4 Appli	ì		4 7 0	18,	Sequence 16, Appl
		QI .	US-09-252-991A-31367	US-09-328-352-6452	US-09-252-991A-31385	US-09-328-352-7248	US-09-328-352-7581	US-09-252-991A-25088	US-09-252-991A-17164	US-09-328-352-4700	US-09-252-991A-19627	US-09-004-393B-4	US-09-004-393B-2	US-08-810-009-19	US-08-810-009-20	US-08-810-009-21	US-09-252-991A-27100	US-09-328-352-6765	US-08-976-063E-4	US-09-028-934-36	US-08-810-009-12	US-08-810-009-14	US-08-810-009-13	US-08-810-009-15	US-09-311-626B-4	113-08-810-009-9	TG-06-300-360-4000	110.09-510-552-4956	8T-600-0T0-00-00	US-08-809-326A-16
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de	Query	Match	17.2	17.1	16.2	16.1	15.1	14.3	12.1	11.6	9.	o,	6.9	7.7	7.2	7.0	9	ω.	4.9	4.8	4.6	4.5	4.5	4.5	4.0	4.4	4	. 4	•	4.5
		Score	415.5	412.5	390.5	388	364	345.5	292	279.5	237.5	224	223	185	174	168	143.5	128	118.5	116.5	110	109	108	108	108	106	106	100		103.3
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, Appl	Appl.	Appl	Appl	. Appl	Appl	Appl	. Appl	Appli	Appl	Appl	Appl		Appl	Appl	6. App	371. A	Appl
16	16	16	15	15	15	15	H	8	7	4	45			57	46	20	46
Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sequence	Seguence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence
US-09-689-914A-16	US-09-689-913A-16	US-09-689-916A-16	US-08-809-326A-15	US-09-689-914A-15	US-09-689-913A-15	US-09-689-916A-15	US-08-810-009511	US-08-810-009-8	US-08-810-009-10	US-08-810-009-44	US-08-810-009-45	US-09-328-352-5961	US-08-810-009-17	US-09-325-932A-57	US-09-198-452A-466	US-09-252-991A-28371	US-08-810-009-46
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ALIGNMENTS

US-09-252-991A-31367

Query Match Best Local Similarity 29.3%; Pred. No. 4.3e-31; Matches 111; Conservative 69; Mismatches 148; Indels 51; Gaps 17;	23 DEBLFQHELKTIFARNWLFLTHDSDIPAPGDYVFAKMGIDEVIVSRQNDGSIRAFLNVCR 82	38 DPRIFEIEMKHIFEGNWYLAHESQVAGVNDYLTTQIGRQSIVIARNEDGQLNAFINACS 97	KTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFFKDLYGESLNKKCLGLKE 137	98 HRGAMLCRHKSGNRSSYTCPFHGWTFNNSGKLLKVKDPAEAG-YPQSFNCEGSHDLTR 154	138 VARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHS-GGLELVGPPGKVVIKANWK 196	: : : : : : :	197 APABNFVGDAYHVGWTHASSLKSGESIFSSLAGNAALPPEGAGLQ 241	215 LTAEN-GADGYHVSSVHWNYAATQSQRQQRDAADPLRTMSAAGWARQGGGFY 265	242 MISKYGSGMGVLWDGYSGVHSADLVPR-LMAFGGAKQBRLNKEIGDVRAR-IYRSHLNCT 299	266SFEHGHMLLWSRWANPEDRPAPERRABLARDFGEARADWMIENSRWIC 313
similar 11, Con	DEBLFO	DPRLFE	HRGKTL	HRGAML	VARVES	VARFES	APAENE	LTAEN	MTSKYG	SFE
Query Match Best Local Matches 11										
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Sequence 7248, Application US/09328352
Patent No. 6562958
GEREAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BADWANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERSACE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
SEQ ID NOS: 8252
SEQ ID NO 7248
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                                                                                                                                                                                                                                                                                                                            83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSV--PFEKDLYGESLNKKCLGLKEVAR 140
                                                                                                                                                                                                                                                                                                                                                                                      141 VESFHGFIYGCFDQEA-PPLADYLGDAAWYLEPMFKH--SGGLELVGPPGKVVIKANWKA 197
                                                                                                                                                                                                                                                                                                                                                                                                                  198 PAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMT---SKYGSGMGVL- 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 QNENGL-DGYHVSTVHYNYV----ATVQHRQQVEAERGGVAATLDYSKLGAGDAATD 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 --WDGYSGVHS------ADLVPELMAFGGAKQERLNKEIGDVRARIYRSHL 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        297 -NCTVPPNNSML-TCSGVFKVMNPIDANTTBVWTYAL-VEKDMPEDLKRRLADSVQRTFG 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 VSGMGTPDDLVZFREAQRGFQARLERWSDI--SRGHGKWLEGATPNSQALGIAPLLTGTE 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 VCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVA 139
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                                                                                                                                                                                                                                 23 DEELFOHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 354 PAGFWESDDNDNMETASONGKKYOSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAI---GE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 RCRHRAATVCEHKKGKTNSFVCPYHGMSYALDGSLRGVP-SPESYGDCLDKSELPLVSL-
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                                                                                                                                                                     Gaps
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                                                                                                               Query Match 16.2%; Score 390.5; DB 4; Length 466; Best Local Similarity 27.4%; Pred. No. 1e-28; Matches 121; Conservative 77; Mismatches 181; Indels 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.1%; Score 388; DB 4; Length 445; 28.1%; Pred. No. 1.7e-28; Live 66; Mismatches 164; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 TSYRGFYRAYQAHVSSSNWAEF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               433 ITHEGLYVNOHAH-----WRRF 449

j TYPE: PRT
j ORGANISM: Acinetobacter baumannii
US-09-328-352-7248

                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 28.1%
Matches 124; Conservative
                                                          ; OKGANISM: Pseudo:
US-09-252-991A-31385
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                                                                                                                                                Sequence 6452, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION: USCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6452
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 31385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 WIQMANPEDRPNFP-----KADEYTEKYGEAMSKWHIERSR-NLCLYPNVYLMDQFG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 SQIRVLRPLSVNRTEVTIYCIAPKGEAPEARARRR-QYEDFRASGMATPDDLEBFR-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.1%; Score 412.5; DB 4; Length 496; 30.8%; Pred, No. 9.2e-31; iive 62; Mismatches 163; Indels 27
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// Patent No. 6551795
                           374 TPDDLEEFRSCQQG---YQ 389
                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-6452
359 ESDDNDNMETASQNGKKYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 112; Conservative
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Best Local Similarity
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US-09-252-991A-31385
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLING DATE: 1999-02-18

PRIOR PLING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17164, Application US/09252991A
Patent No. 651795
GENERAL INCEMENTION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPRESENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S-----ADLVPE-LMAFGGAKQERLNKEIGDVRAR-IYRSHLNCTVFPN---N 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 SGPPSTGRPIAYWSPLFPEALKPSIAAKFERLVERFGQARAEDIAHTWKSLFIFPNIVIN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 SMLTCSGVFKVWNPIDANTTEVWTYALVEKOMPEDLKRRLADSVORTFGPAGFWESDDND 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      307 DILGIN--IRSFFFFRAADEVSVIVWGAGFADETREERAARINGLISFIGPGGFGTPDDVE 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 VYRNFLFIHYAARQPSLETYLGQAKDYIDLICDQSEAELBIIPGGFEHSIKANWKLLABN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQNDGSIRAFLNVCRHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 NMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 14.3%; Score 345.5; DB 4; Il Similarity 27.4%; Pred. No. 1.8e-24; 114; Conservative 71; Mismatches 178;
                                                                                                                                                                           Sequence 25088, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas aeruginosa
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                                                                                                                                      RESULT 6
US-09-252-991A-25088
                                419 AYQAH
                                                                       437 NOHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Pseudo
US-09-252-991A-25088
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Best Local S:
Matches 114,
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Batent No. 6562958

BAREAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GFC99-03PA
CURRENT FILLING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7581
                                                            193 ANWKAPAENFVGDAYHVGWTHASSLRS----GESIFSSLAGNAALPPEGAGLQWTSKYGS 248
                                                                                                                                                                                                                             ---SHINCTVEPNNSMLICS-GVFKVMNPIDANTTBVWTYAIVEXD----MPEDLKRRLA 345
                                                                                                                                             GMGVLWDGYSGVHSADLVPELMAFGGAKQER-LNKEIGDVR------ARIYR- 293
                                                                                                                                                                         318 VGGSGPALALFPN---IACSMAPFRVLQPISVAETEI-HHSVITWDGGPQIANQYRLRLH 373
                                                                                                                                                                                                                                                                                                                                            ST4 EHFQ---GPRCFGTPDDSEAMERV-QHGAN-AGNDLWIMLINRGL------PGEVKT 418
                                                                                                              -----FBN 257
                                                                                                                                                                                                                                                                                                             DSVQRTFGPAGFWESDDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVG- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEXDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143 SPHGFIYGCPDQEA-PPLMDYLGDAAWYLEPMFKHS--GGLELVGPPGKYVIKANWKAPA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 RNFVGDAYHVGWTH---ASSLRSGESIFSSLAGNAALPPEGAGLOMT--SKYGSGMGVLW 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGYSGVHSADLV-----PELMAFGGAKQERLNKBIGDVRARIYRSHL-NCTVFPNNSM 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 DGWFSFKNGHSVLFSDMPNPTVRPGYSTVMPYMVEKYGEKYABWAMHRIRNINLYPSIFP 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 L-TCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTFGFAGFWESDDNDN 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323 MDQISSQLRIVRPVAMNKTEVISQCIGVKGESTEARRNRIRQFEDFFNVSGLGTPDDLVE 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 METASQNGKKYQSRDSDLLSNLGFGEDVYGD-----AVYPGVVGKSAIGETSYRGFYR 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    383 FREQOKGFQARLERWSDI--SRGCQSWEYGATKNSQDLGIQPVITGR----EFTHBGLIV 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 DEELFQHELKTIFARNWLFLTHDSILPAPGDYVTARMGIDEVIUSRQNDGSIRAFLNVCR 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15,1%; Score 364; DB 4; Length 471; Best Local Similarity 27,1%; Pred. No. 3.6e-26; Matches 115; Conservative 67; Mismatches 201; Indels
                                                                                                   -NWKIQLEN-TTDAYHFPLVHKSFLSSVDEKTEELFN--
                                                                                                                                                                                                                                                                                                                                                                                                                              419 BDGLKSDVSAETGMRAAYQQWK 440
                                                                                                                                                                                                                                                                                                                                                                                                  ----KSAI-GETSYRGFYRAYQ 421
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TYPE: PRT:
i ORGANISM: Acinetobacter baumannii
.US-09-328-352-7581
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENITON: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENITON: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENITON: AEROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ. ID NOS: 33142.
SEQ. ID NO 19627
           131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVV 190
                                                                                                    191 IX--ANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGS 248
                                                                                                                                                 ---- PGFADSVQVDKYWH 231
                                                                                                                                                                                                 ---PNNS 305
                                                                                                                                                                                                                                       232 TTHONWILOYG------PARSSEKSFKLDPSVTDPEFHGFWT-WPCTMFNVPPGSN 280
                                                                                                                                                                                                                                                                                                               149 YGCFDQBAPPIMDYLGDAAWYLEPMFKHSGGLE--LVGPPGKVVIKANWKAPAENFVGDA 206
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                                        : | : | : : : : : | : | 141 SMVPLK----VESYAGFVFINMDENATCVEDQL---PGFAERLNQACGVIKDLKLAARFV
                                                                                                                                                                                                                                                                                  306 MLTCSGVFKVWNPIDANTIEVWTYAIV-----EKDM-----PEDLKRRLADS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          231 QTECTGQRPLVCPYHAMSFGARGQLQGIP-NSSLYQFSAEBRARIGLRKL-HIBEVGQLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 FVNLADDPLPLREQEDDG--FLETLREVSSHLDTRLIYSCHKV--RYNWKLINMEN-VKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 WFSDLCEGYGDEH-----AYYNWFIYPDNVNFCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 BLKTIFARNALFLTHDSLIPAPGDYVTAKMGIDEVIVSRONDGSIRAFLNVCRHRGKTLV
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                                                                                                                                                                                          249 GMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTVF
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9.9%; Score 237.5; DB 4; Length 5
Best Local Similarity 24.9%; Pred. No. 4.7e-14;
Matches 86; Conservative 54; Mismatches 139; Indels
                                                                                                                              Sequence 19627, Application US/09252991A Patent No. 6551795
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19627
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US-09-252-991A-19627
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Patent No. 6562958

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPERENCE: GT-09-039A
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                                                                                                                                                                                                                                                                     |: ||: ::: || : : || DORLFBIDMQBIFHKEWLIAGMTCEIPAKGNFLTLQIGKOPVLVIRGAEGQVHAFHNVCR 119
                                                                                                                                                                                                                                                                                                                                                                                                                   HRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVE 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 SFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGLELVGPPGKVVIK-----ANWK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197 APAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPEGAGLQMTSKYGSGMGVJWDG 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257 YSGVHSADLVPELMA-FG----------GAKQ---ERLNKEIGDVRA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 RIYRSHLNCTVFPNNSMLTCSG----VFKVWNPIDANTTEVMTYAIVEKDMPB----- 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 -----DLKRRIADSVORTFGPAGFWESDDNDNNETASQNGKKYQSRDSDLLSNLG 388
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                                                                                                                                                                                                                                                                                                                        23 DEBLPOHELKTIFARNWLFLTHDSLIPAPGDYVTAKWGIDEVIVSRQNDGSIRAFLNVCR
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                                                                                                                                                                                                                                                                                     96;
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11.6%; Score 279.5; DB 4; Length 375;
Best Local Similarity 26.2%; Pred. No. 2.8e-18;
Matches 97; Conservative 57; Mismatches 131; Indels 85
                                                                                                                                                                                                                              Query Match
12.1%; Score 292; DB 4; Length 449;
Best Local Similarity 26.4%; Pred. No. 2.4e-19;
Matches 111; Conservative 53; Mismatches 160; Indels
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17164
LENGTH: 449
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US-09-328-352-4700
                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                   US-09-252-991A-17164
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US-09-328-352-4700
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LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99 EDALTPPSTWYTEPARYSHELERIFYKGWQVAGYSEQVKEKNQYFTGSLGNVEYLVSRDG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 DGSIRAFLNYCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 KCLGLKEVARVESFHGFIYGCFDQEAPPLMD----YLGDA----AWYLEPMFKHSGGLE 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 ESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMGIDEVIVSRQN 70
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APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapath, Bala
APPLICANT: Rathinasabapath, Bala
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Polynucleotides Encoding Choline Monocxygenase and
TITLE OF INVENTION: Plants Transformed Therewith
FILE REFERENCE: UF-162
CURRENT APPLICATION NUMBER: US/09/004,3938
CURRENT FILING DATE: 1990-01-08
FRIOR FILING DATE: 1997-01-08
SHORE RELING DATE: 1997-01-08
SHUMBER OF SEQ ID NOS: 6
                                                                                         APPLICANT: Hanson D., Andrew
APPLICANT: Rathinasabapathi, Bala
APPLICANT: Burnet, Michael
APPLICANT: Burnet, Michael
TITLE OF INVENTION: Plants Transformed Therewith
TITLE OF INVENTION: Plants Transformed Therewith
TITLE OF INVENTION: Plants Transformed Therewith
TITLE OF INVENTION: 109-10.
CURRENT APPLICATION NUMBER: 1099-01-08
FRIOR PAPLICATION NUMBER: 60/035,147
PRIOR PLIING DATE: 1997-01-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.3%; Score 223; DB 4; Length 439;
Best Local Similarity 30.1%; Pred. No. 8.6e-13;
Matches 58; Conservative 38; Mismatches 83; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.3%; Score 224; DB 4; Length 446; Best Local Similarity 27.4%; Pred. No. 7.1e-13; Matches 58; Conservative 37; Mismatches 97; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 F-----PMECNWKVFCDNYLDSSXHVPYAH 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 LVGPPGKVVIKANWKAPAENPVGDAYHVGWTH 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/09004393B
Patent No. 6310271
               Sequence 4, Application US/09004393B Patent No. 6310271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Ver. 2.0
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U8-09-004-393B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Beta vulgaris
                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pat.
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US-09-004-393B-2
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US-09-004-393B-4
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87 TLVSVEAGNAKGFVCSYHGWGFGSNGELQSVPFEKDLYGESLNKKCLGLKEVARVESFHG 146
                         167 SILACGSGKKSCFVCPYHGWYGMDSLAKASKAKP--EQNLDPKELGLVPL-KVAVWGP 223
                                                                                                    147 FIYGCFDQEAPPLMD----YLGDAAWYLEPMFKHS--GGLELVGPPGKVVIKANWKAPAE 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
TITLE OF INVENTION: CELL DEATH AND DISEASE RESISTANCE IN PLANTS
CORRESPONDENCES: 65
CORRESPONDENCES ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
AJTONEN/AGENT INFORMATION:
NAME: Spruill, W. Multray
REGISTRATION NUMBER: 32,943
REGISTRATION NUMBER: 32,943
REGISTRATION INFORMATION:
TELEPRAK: 919-881-3175
TELEPAK: 919-881-3175
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APPLICANT: Briggs, Steven P.
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 19, Application US/08810009; Patent No. 6211437; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   201 NFVGDAYHVGWTH 213
                                                                                                                                                                                                                                                   280 NYLDSSYHVPYAH 292
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US-08-810-009-19
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Patent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Johal, Gurmukh S.
CORRESPONDENCE ADDRESS:
ADDRESSER: BELL, SELTZER, PARK & GIBSON
CITY: Charlotte
CITY: Charlotte
STATE: No. 6211437th Carolina
COUNTRY: USA
APPLICANT: Johal, Gurmukh S.
APPLICANT: Johal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
TITLE OF INVENTION: CELL, DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS: 65
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITT Charlotte
STREET: Charlotte
STRYE: No. 611437th Carolina
COUNTRY: USA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE: US/08/810,009
FILING DATE: 04-MAR-1997
                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM FC compatible
COMPUTER: IEM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CHRENT APPLICATION DATA:
APPLICATION NAMER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIPICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 575102
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MOLECULE TYPE: protein
US-08-810-009-20
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US-08-810-009-21
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Sequence 27100, Application US/09252991A
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA DA DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ASSUGINOSA DA DIAGNOSTICS AND THERAPEUTICS
CURRENT PILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 27100
LENGTH: 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 GIDEVIVSRONDGSIRAFLAVCRHRGK--TIVSVEAGNAKGFVCSYHGWGFGSNGELQSV 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 CDEPMYFYRGEDGRVAALEDFCPHRGAPLSLGFVEDG---VLVCGYHGLAMGEDGRTRAM 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 PFEKOLYGESLNKKCLGLKEVAR--VESFHGFIY---GCFDGEAPPLMDYLGDAAWYLEP 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 168; DB 3; Length 35;
80.0%; Pred. No. 3.2e-09;
tive 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 NVCRHRGKTLVSVEAGNAKGFVCSYHGWGFGSNGE 113
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               ATTORNEY/AGENT INFORMATION:
NAME: SPINILI, W. WINTRAY
REGISTRATION NUMBER: 32 943
REFERENCE/DOCKET NUMBER: 5718:
TELECHONICATION INFORMATION:
TELECHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rype: PRT cordanism: Pseudomonas aeruginosa US-09-252-991A-27100
                                                                                                                                                                                         TELEX: 575102
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 80.0
nes 28; Conservative
                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                               amino acid
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           US-08-810-009-21
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Matches
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Search completed: December 9, 2003, 15:45:52 Job time : 12 secs

December 9, 2003, 15:44:14; Search time 22.1429 Seconds (without alignments) 3771.269 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM protein - protein search, using sw model US-09-843-250-2 Perfect score: Run on:

BLOSUM62 Scoring table: Sequence:

684280 seqs, 185983659 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

Ggn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(Ggn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

(Ggn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

(Ggn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

(Ggn2_6/ptodata/1/pubpaa/PGTUB_PUBCOMB.pep:*

(Ggn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

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(Ggn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		09-843	09-843	.09-843	09-843	0.00	2010	09-843	09-843	CA8-90		09-643	09-843	09-843		09-843	09-843		09-843	JS-09-843-250-19
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	DB	Ħ	11	11	15	;	•	ä	#	-	:	4	검	1	,	=	11	•	7	11
	Length	449	449	449	449	449		449	449	449		444	449	449		44	449	417	44	449
Query	Match	100.0	100.0	100.0	100.0	0		y.	99.8	8.66			99.8	99.7			93.6		0	96.4
	Score	2408	2408	2408	2407	2405		4047	2404	2403	2403	2 4	2403	2401	20.00	7047	2398	0000	000	2322
Result	No.	н	7	ო	4	ហ		0		80	a	•	70	=======================================	c	7 :	13	74		15
	•	Query Score Match Length DB	Score Match Length DB ID Description 2408 100.0 449 11 US-09-843-250-2	Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-2 2408 100.0 449 11 US-09-843-250-3	Score Match Length DB ID Description 2408 100.0 449 11 US-09-843-250-2 Sequence 2, 2408 100.0 449 11 US-09-843-250-14 Sequence 14 2408 100.0 449 11 US-09-843-250-14	Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-2 2408 100.0 449 11 US-09-843-250-14 Sequence 2, 2407 100.0 449 11 US-09-843-250-15 Sequence 15	Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-2 Sequence 12 2408 100.0 449 11 US-09-843-250-14 Sequence 14 2408 100.0 449 11 US-09-843-250-15 Sequence 15 2407 100.0 449 11 US-09-843-250-15 Sequence 15 2407 100.0 449 11 US-09-843-250-15 Sequence 36 2407 100.0 449 11 US-09-843-250-36 Sequence 36	Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-15 2408 100.0 449 11 US-09-843-250-15 2407 100.0 449 11 US-09-843-250-15 2407 100.0 449 11 US-09-843-250-36 2405 99.9 449 11 US-09-843-250-36 Sequence 36 2405 99.9 449 11 US-09-843-250-36 Sequence 36	Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-2 Sequence 2, 2408 100.0 449 11 US-09-843-250-14 Sequence 15 2408 100.0 449 11 US-09-843-250-15 Sequence 15 2405 100.0 449 11 US-09-843-250-35 Sequence 35 2404 99.8 449 11 US-09-843-250-35 Sequence 35 2404 99.8 449 11 US-09-843-250-35 Sequence 35 2404 99.8 449 11 US-09-843-250-35	Query Query Description 2408 100.0 449 11 US-09-843-250-2 Sequence 2, A Sequence 2, A Sequence 2, A Sequence 14, 2408 100.0 449 11 US-09-843-250-14 Sequence 14, Sequence 15, 2407 100.0 449 11 US-09-843-250-15 Sequence 15, Sequence 36, 2407 100.0 449 11 US-09-843-250-36 Sequence 36, Sequence 36, Sequence 36, Sequence 36, Sequence 37, Sequence 37, Sequence 37, Sequence 38, Sequence 38, Sequence 37, Sequ	Query Query Score Match Length DB ID Description 2408 100.0 449 11 US-09-843-250-2 Sequence 2, AS-408 Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 14, Sequence 15, Sequence 15, Sequence 15, Sequence 15, Sequence 35, Sequence	Query Query Score Match Length DB ID Description 2408 100.0 449 11 US-09-843-250-2 Sequence 2, Agenore 14, 240 2408 100.0 449 11 US-09-843-250-15 Sequence 14, 240 2408 100.0 449 11 US-09-843-250-15 Sequence 15, Sequence 36, 240 2405 99.9 449 11 US-09-843-250-36 Sequence 35, Sequence 35, 2404 2404 99.8 449 11 US-09-843-250-34 Sequence 33, Sequence 34, 240 2403 99.8 449 11 US-09-843-250-34 Sequence 34, 240	Query Query Core Match Length DB ID Description 2408 100.0 449 11 US-09-843-250-2 Sequence 2, AS-408 Sequence 14, Sequence 15, Sequence 35, Sequence 36, Sequence	Query Query 2408 100.0 449 11 US-09-843-250-2 Sequence 2, A Sequence 2, A Sequence 2, A Sequence 3, A Sequence 14, A Sequence 14, A Sequence 15, A Sequence 15, A Sequence 15, A Sequence 16, A Sequence 36,	Query Query 2408 100.0 449 11 US-09-843-250-2 Sequence 2, B. 2408 100.0 449 11 US-09-843-250-14 Sequence 14, Sequence 14, Sequence 15, 2408 100.0 449 11 US-09-843-250-15 Sequence 15, Sequence 15, 2407 100.0 449 11 US-09-843-250-15 Sequence 15, Sequence 15, Sequence 36, Sequence 36, Sequence 36, Sequence 37, Sequence 26, Sequence 16, Sequence 16, Sequence 16, Sequence 26, Sequence	Query Query 2408 100.0 449 11 US-09-843-250-2 Sequence 2, A Sequence 2, A Sequence 2, A Sequence 3, A Sequence 14, A Sequence 14, A Sequence 15, A Sequence 15, A Sequence 15, A Sequence 16, A Sequence 36, A Sequence 37, A Sequence 37, A Sequence 37, A Sequence 37,	Query Query 2408 Match Length DB ID 2408 100.0 449 II 2408 100.0 449 II US-09-843-250-1 Sequence 2, Asquence 14, 100.0 2408 100.0 449 II US-09-843-250-15 Sequence 15, Sequence 15, 240.7 2407 99.8 449 II US-09-843-250-36 Sequence 35, Sequence 35, Sequence 35, Sequence 37, 240.4 2403 99.8 449 II US-09-843-250-36 Sequence 37, Sequence 16, Sequence 16, Sequence 16, Sequence 16, Sequence 26, Sequence 27, Sequence 26, Sequence 27, Sequence 26, Sequence 59, Sequence 50,	Query Query 2408 100.0 449 11 US-09-843-250-2 Sequence 2, August 100.0 449 11 US-09-843-250-14 Sequence 14, Sequence 2, August 100.0 449 11 US-09-843-250-15 Sequence 15, Sequence 15, Sequence 16, Sequence 16, Sequence 36, Sequence 37, Sequence 16, Sequence 17, Sequence 17, Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 26, Sequence 37, Sequen	Query Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-14 2408 100.0 449 11 US-09-843-250-14 2408 100.0 449 11 US-09-843-250-15 2407 100.0 449 11 US-09-843-250-15 2407 100.0 449 11 US-09-843-250-15 2404 99.8 449 11 US-09-843-250-35 2404 99.8 449 11 US-09-843-250-35 2403 99.8 449 11 US-09-843-250-16 2403 99.8 449 11 US-09-843-250-16 2403 99.8 449 11 US-09-843-250-16 2401 99.7 449 11 US-09-843-250-59 2401 99.7 449 11 US-09-843-250-37 2401 99.8 410 US-09-843-250-37 2401 99.8 410 US-09-843-250-37 2401 99.8	Score Match Length DB ID 2408 100.0 449 11 US-09-843-250-2 2408 100.0 449 11 US-09-843-250-15 2408 100.0 449 11 US-09-843-250-15 2408 100.0 449 11 US-09-843-250-15 2401 100.0 449 11 US-09-843-250-15 2404 99.8 449 11 US-09-843-250-36 2404 99.8 449 11 US-09-843-250-36 2404 99.8 449 11 US-09-843-250-36 2403 99.8 449 11 US-09-843-250-26 2401 99.7 449 11 US-09-843-250-26 2401 99.7 449 11 US-09-843-250-39 2550 97.6 449 11 US-09-843-250-38 Sequence 59 Sequence 59

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9 9 1 MNYNNKILVSESGLSQKHLIHGDEBLFQHELKTIFARNMLFLTHDSLIPAPGDYVTAXMG 1 MNYNNKILVSESGLSQKHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAFGDYVTAKMG

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Sequence 20, Appl	Sequence 21, Appl	22	23		10253	Sequence 6140. An	Sequence 11692. A	Seguence 5097. Ap			Sequence 19. Appl	20.	Sequence 20. Appl	21.	Sequence 21. Appl	4	Sequence 12. Appl	12	14	14	4	13	15	133	15		-	6	
11 US-09-843-250-20	11 US-09-843-250-21	11 US-09-843-250-22		11 US-09-843-250-24	₽	10 US-09-738-626-6140	9 US-09-815-242-11692	9 US-09-815-242-5097	15 US-10-156-761-14477	9 US-09-776-490-19	9 US-09-776-491-19	9 US-09-776-490-20	9 US-09-776-491-20	9 US-09-776-490-21	9 US-09-776-491-21	8 US-08-976-063C-4	9 US-09-776-490-12	9 US-09-776-491-12	9 US-09-776-490-14	9 US-09-776-491-14	15 US-10-124-880-4	9 US-09-776-490-13	9 US-09-776-490-15	9 US-09-776-491-13	9 US-09-776-491-15	14 US-10-047-542-78	10 US-09-924-097-15	9 US-09-776-490-9	9 US-09-776-491-9
449	449	447	447	451	453	490	385	424	382	35	35	35	32	35	32	354	32	35	35	35	622	32	35	35	35	548	951	35	35
95.3	92.3	91.1	85.4	81.9	30.6	15.6	15.6	14.1	10.2	7.7	7.7	7.2	7.2	7.0	7.0	4.9	4.6	4.6	4.5	4.5	4.5	4.5	4. T	4.5	4.5	4.5	4	4.4	4.4
2296	2223	2193	2056	1972.5	736	376	375.5	340.5	245.5	185	185	174	174	168	168	118.5	110	110	109	109	109	108	108	108	108	107.5	106.5	106	106
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 2, Application US/09843250

Publication No. US2003002233541

GENERAL INPORMATION:

APPLICANT: Parales, R.

APPLICANT: Gibson, D.

APPLICANT: Reenick, S.

APPLICANT: Lee, K.

TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006US2

CURRENT PELICATION NUMBER: US/09/843,250

CURRENT FILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR PILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

PRIOR FILING DATE: 1998-10-26

SOFTWARE FILING DATE: 1998-10-26

SOFTWARE FILING DATE: 1998-10-26

SOFTWARE FILING DATE: 1998-10-26

SOFTWARE FILING DATE: 1998-10-26

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 2

LENGTH: 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 2.6e-226;
Matches 449; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:1
US-09-843-250-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
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	MO. US200300 006052 2001-04-28 40ER: PCT/US 999-10-26 998-10-26 65 F Windows Ve Windows Ve 1 Sequence	PAPGI	100.0%; Score 2408; DB 11; Length 449; b) conservative 0; Mismatches 0; Indels 0; Gaps 0; Conservative 0; Mismatches 0; Conservative 0	181 BLVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPBGAGL	
TYLER 			Length 4 ndels THDSLIPA		

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Squence 35, Application US/09843250

Fublication No. US20030022335A1

GENERAL INFORMATION:

FUBLICALT: Parales, R.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

APPLICANT: Resnick, S.

TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPERENCE: 875.006US2

CURRENT FILING DATE: 2001-04-26

FRIOR APPLICATION NUMBER: US/09/843,250

CURRENT FILING DATE: 1999-10-26

FRIOR APPLICATION NUMBER: US 60/105,575

FRIOR FILING DATE: 1998-10-26

FRIOR FILING DATE: 1998-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE PARENCE: PARENCE: PARENCE: PRIOR PARENCE: PARENCE: PRIOR PARENCE: PAREN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 QMTSKYGSGWGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 QMTSKYGSGMGVLWDGYSGVHSADLVPELMAFGGAKQERLNKEIGDVRARIYRSHLNCTV 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.9%; Score 2405; DB 11; Length 449; 99.8%; Pred. No. 5.1e-226; ive 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:30
US-09-843-250-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.8 Matches 448; Conservative
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: Parales, R.
APPLICANT: Barales, R.
APPLICANT: Gibson, D.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REPERENCE: 875.006US22
CURRENT FILING DATE: 1006US22
CURRENT FILING DATE: 1009-10-26
PRIOR PILING DATE: 1099-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 36
LENGTH 449
IDEVIVSRONDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGWGRGSNGELOSVPFE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IDBVIVSRQNDGSIRAFLAVCRHRGKTLVSVEAGNAKGFVCSYHGMGFGSNGBLQSVPFB 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KDLYGESLANKKCLGLKEVARVESFHGFIYGCFDQEAPPLMDYLGDAAWYLEPMFKHSGGL 180
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100.0%; Score 2407; DB 11; Length 449;
Best Local Similarity 99.8%; Pred. No. 3.2e-226;
Matches 448; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:31 US-09-843-250-36
                                                                                                                      QAHVSSSNWAEFEHASSTWHTELTKTTDR 449
                                                                                    OAHVSSSNWAEFEHASSTWHTELTKTTDR 449
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                                                                                                                                                                                                                                                                            ; Sequence 36, Application US/09843250; Publication No. US20030022335A1; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-843-250-36
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APPLICANT: Parales, R.
APPLICANT: Barales, R.
APPLICANT: Gibson, D.
APPLICANT: Resultck, S.
APPLICANT: Resultck, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for their rights of INVENTION NUMBER: US/09/843,250
CURRENT FILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PARIESEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 449
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; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:29. US-09-843-250-34
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US-09-843-250-16
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Pred. No. 6.4e-226;
0; Mismatches 1;
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Publication No. US20030022335A1
GENERAL INFORMATION:
               SEQ ID NO 34
LENGTH: 449
TYPE: PR:
ORGANISM: Artificial Sequence
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Best Local Similarity 99.8%;
Matches 448; Conservative
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ORGANISM: Artificial Sequence
PRATURE:
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US-09-843-250-16
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Publication No. US20030022335A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Parales, R.
APPLICANT: Perales, R.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE OF INVENTION: NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 1999-10-4-26
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
PRIOR PLING DATE: 1999-10-26
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Pred. No. 6.4e-226;
0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:28.
US-09-843-250-33
FILE REFERENCE: 875.006US2
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PSESSEQ for Windows Version 4.0
SENGTH: 449
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 99.8%;
Matches 448; Conservative
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APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Parales, R.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE NO INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REFERENCE: 875.006USZ
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT APPLICATION NUMBER: PCT/US99/25079
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR FILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOFTMARE: PareLEGG for Windows Version 4.0
SEQ ID NO 59
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                                                                                                                                                                                                                                               ; OTHER INFORMATION: A polypeptide encoded by SEQ ID NO:57.
US-09-843-250-59
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ORGANISM: Artificial Sequence
FEATURE:
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| Publication No. US20030022335A1
| GENERAL INFORMATION:
| APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the FILE REPRENEURS: 875.006US2
| CURRENT PELICATION: No. US20030022335A1e1 naphthalene dioxygenase and methods for the CURRENT PELICATION: WS/09/843,250
| CURRENT PILING DATE: 2001-04-26
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                                                                                    1 MNYNNKILVSESGLSQKHLIHGDESELPQHELKTIFARNWLPLTHDSLIPADGDYVTAKYG 60
                                                             1 MAYNINKILYSESGLSQXHLIHGDEELFQHELKTIFARNWLFLTHDSLIPAPGDYVTAKMG 60
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99.8%; Fred. No. 8e-226;
tive 0; Mismatches 1; Indels
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PRIOR FILING DATE: 1999-10-26
PRIOR FILING DATE: 1999-10-26
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PRESEQ for Windows Version 4.0
LENGTH: 449
Best Local Similarity 99.84
Matches 448; Conservative
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US-09-843-250-26
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US-09-843-250-26
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APPLICANT: Parales, R. APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Galson, D. APPLICANT: Remaick, S. APPLICANT: Lae, K. TITLE OF INVENTION: No. U$20030022335Alel naphthalene dioxygenase and methods for the: FILE REPERENCE: 875.006032 CURRENT APPLICATION NUMBER: U$/09/843,250 CURRENT PILING DATE: 2001-04-26 PRIOR APPLICATION NUMBER: U$ (0/105,575 PRIOR PILING DATE: 1998-10-26 NUMBER OF SEQ ID NOS: 65 SOFTWARB: FastSEQ for Windows Version 4.0 SEQ ID NO 58
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361 DDNDNMETASQNGKKYQSRDSDLLSNLGFGEDVYGDAVYPGVVGKSAIGETSYRGFYRAY 420
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US-09-843-250-58
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                                                                      421 QAHVSSSNWABFEHASSTWHTELTKTTDR 449
                                                                                                                                                                                                                                                                                                                  Sequence 58, Application US/09843250 Publication No. US20030022335A1 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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US-09-843-250-17
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   241 QMISKYGSGAGVLMDGYSGVHSADLVPBLMAFGGAKQERLNKEIGDVRARIYRSHINCTV 300
                                                                                                              PPINSMLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES 360
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99.7%; Score 2401; DB 11; Length 449;
Best Local Similarity 99.8%; Pred. No. 1.2e-225;
Matches 448; Conservative 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/09843250 Publication No. US20030022335A1 GENERAL INFORMATION:
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Gequence 19, Application US/09843250

Fublication No. US20030022335A1

GENERAL INFORMATION:

APPLICANT: Parales, R.

APPLICANT: Remick, S.

APPLICANT: Lee, R.

TITLE OF INVENTION: No. US20030022335A1c1 naphthalene dioxygenase and methods for the TITLE OF INVENTION: No. US20030022335A1c1 naphthalene dioxygenase and methods for the FILE REPRENCE: 875.006US2

CURRENT PLILING DATE: 2001-04-26

PRIOR PRILING DATE: 1999-10-26

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR APPLICATION NUMBER: US 60/105,575

PRIOR FILING DATE: 1999-10-26

NUMBER OF SEQ ID NOS: 65

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 19
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US-09-843-250-18
CURRENT APPLICATION NUMBER: US/09/843,250
CURRENT FILING DATE: 2001-04-26
PRIOR APPLICATION NUMBER: PCT/US99/25079
PRIOR PILING DATE: 1999-10-26
PRIOR APPLICATION NUMBER: US 60/105,575
PRIOR PILING DATE: 1998-10-26
NUMBER OF SEQ ID NOS: 65
SOPTWARE: PRESEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 449
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US-09-843-250-19
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                                                                                              APPLICANT: Parales, R. APPLICANT: Parales, R. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Gibson, D. APPLICANT: Resnick, S. APPLICANT: Lee, K. TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the FILE REPERENCE: 975-006US2. CURRENT FILING DATE: 2001-04-26 PRIOR PILING DATE: 1999-10-26 PRIOR FILING DATE: 1999-10-26 PRIOR FILING DATE: 1999-10-26 PRIOR FILING DATE: 1998-10-26 PRIOR 
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APPLICANT: Parales, R.
APPLICANT: Gibson, D.
APPLICANT: Resnick, S.
APPLICANT: Resnick, S.
APPLICANT: Lee, K.
TITLE OF INVENTION: No. US20030022335Alel naphthalene dioxygenase and methods for the
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US-09-843-250-17
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Sequence 17, Application US/09843250 Publication No. US20030022335A1 GENERAL INFORMATION:
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Best Local Similarity 99.69
Matches 447; Conservative
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181 ELVGPPGKVVIKANWKAPAENFVGDAYHVGWTHASSLRSGESIFSSLAGNAALPPECAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                           181 BLVGPPGKVVIKANWKAPAENPVGDAYHVGMTHASSLRTGESIFSSLAGNAVLPPEGAGL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                               301 FPNNSVLTCSGVFKVWNPIDANTTEVWTYAIVEKDMPEDLKRRLADAVQRTVGPAGFWES 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 PPNNSMLTCSGVEKVWNPIDANTIEVWTYAIVEKDMPEDLKRRLADSVQRTVGPAGFWES 360
                                                                                                                                                                                                            1 MNYNNKILVSESGLSOKHLIHGDEBLPQHELKTIFARNWLFLTHDSLIPAPGDYVTAXMG 60
                                                                                                                                                                                                                              1 MNYKNKILVSESGLTQKHLIHGDBELFQHELRTIXARNWLFLTHDSLIPSPGDYVTAKMG 60
                                                                                                                                                                              0; Gaps
                                                                                                                                                Query Match
Best Local Similarity 95.8%; Pred. No. 6.5e-218;
Matches 430; Conservative 12; Mismatches 7; Indels 0
                                       FEATURE:
CTHER INFORMATION: A polypeptide encoded by SEQ ID NO:8.
NAME/KEY: SITE
COCATION: (35)...(35)
CTHER INFORMATION: Kaa = any amino acid.
US-09-843-250-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 QAHVSSSNWAEFEDASSTWHTELTKTTDR 449
LENGTH: 449
TYPB: PRT
ORGANISM: Artificial Seguence
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Search completed: December 9, 2003, 16:09:30 Job time: 23,1429 sec8